


```
RESULT 2
US-10-810-262-11
; Sequence 11, Application US/10810262
; Publication No. US20040234505A1
; GENERAL INFORMATION:
; APPLICANT: NAVILOR, STUART
; APPLICANT: KINGSMAN, SUSAN MARY
; APPLICANT: BINFLEY, KATIE
; TITLE OF INVENTION: POLYNUCLEOTIDE CONSTRUCTS AND USES THEREOF
; FILE REFERENCE: 674523-2029.1
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/10/810,262
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: PCT/GB99/03181
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/GB98/02885
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: GB 9901906.9
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: GB 9903538.8
; PRIOR FILING DATE: 1999-02-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO: 11
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-810-262-11

Query Match          99.7%; Score 1535; DB 5; Length 303;
Best Local Similarity 99.6%; Pred. No. 6,5e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTNGKNYRGTMSTKNGITCQKMSSTSPHRPFPSPATHPSEGLSENNYCRPN 60
DB 33 VYLSECKTNGKNYRGTMSTKNGITCQKMSSTSPHRPFPSPATHPSEGLSENNYCRPN 92

QY 61 DPGGWCYTTDPBKRKYDVCIDILCEBECMHSGENYDKISKTMSGLBEOANDSQSPH 120
DB 93 DPGGWCYTTDPBKRKYDVCIDILCEBECMHSGENYDKISKTMSGLBEOANDSQSPH 152

QY 121 GYIPSKFPNKNLKNYCRNPDELPRWCFTTDPNKRWEICDIPRCTPPSSGPTYYQCL 180
DB 153 GYIPSKFPNKNLKNYCRNPDELPRWCFTTDPNKRWEICDIPRCTPPSSGPTYYQCL 212

QY 181 GTGENYRGVAVTVSGHTCOHWSAQTPTHTERTPENFPCKNDENYCRNPDGKRAPWCH 240
DB 213 GTGENYRGVAVTVSGHTCOHWSAQTPTHTERTPENFPCKNDENYCRNPDGKRAPWCH 272

QY 241 TNSQVMEYCKIPSCDSSPV 260
DB 273 TNSQVMEYCKIPSCDSSPV 292

RESULT 3
US-09-788-142-3
; Sequence 3, Application US/09788142
; Patent No. US20010029246A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jones & Askew, LLP
; STREET: 191 Peachtree Street, 37th Floor
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1769
; COMPUTER READABLE FORM:
```

```
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/788,142
FILING DATE: 16-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/866,735
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
```

```
US-09-788-142-3
Query Match          99.7%; Score 1535; DB 3; Length 339;
Best Local Similarity 99.6%; Pred. No. 7.4e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 VYLSECKTNGKNYRGTMSTKNGITCQKMSSTSPHRPFPSPATHPSEGLSENNYCRPN 60
DB 1 VYLSECKTNGKNYRGTMSTKNGITCQKMSSTSPHRPFPSPATHPSEGLSENNYCRPN 60

QY 61 DPGGWCYTTDPBKRKYDVCIDILCEBECMHSGENYDKISKTMSGLBEOANDSQSPH 120
DB 61 DPGGWCYTTDPBKRKYDVCIDILCEBECMHSGENYDKISKTMSGLBEOANDSQSPH 120

QY 121 GYIPSKFPNKNLKNYCRNPDELPRWCFTTDPNKRWEICDIPRCTPPSSGPTYYQCL 180
DB 121 GYIPSKFPNKNLKNYCRNPDELPRWCFTTDPNKRWEICDIPRCTPPSSGPTYYQCL 180

QY 181 GTGENYRGVAVTVSGHTCOHWSAQTPTHTERTPENFPCKNDENYCRNPDGKRAPWCH 240
DB 181 GTGENYRGVAVTVSGHTCOHWSAQTPTHTERTPENFPCKNDENYCRNPDGKRAPWCH 240

QY 241 TNSQVMEYCKIPSCDSSPV 260
DB 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 4
US-09-761-120-3
; Sequence 3, Application US/09761120
; Patent No. US20020037847A1
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; APPLICANT: O'Reilly, Michael
; TITLE OF INVENTION: Nucleic Acids Encoding Kringles 1-5 Region Fragments of Plasminogen
; FILE REFERENCE: 05940-0151 (43171-252068)
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US/09/761,120
; PRIOR FILING DATE: 1999-05-11
```

; PRIOR APPLICATION NUMBER: 08/866,735
 ; PRIOR FILING DATE: 1997-05-30
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 339
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-761-120-3

Query Match 99.7%; Score 1535; DB 3; Length 339;
 Best Local Similarity 99.6%; Pred. No. 7.4e-120;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSCKTGNGKNYRGTMKTKNGITTCQKWSSTSPHRPSPATPSGLBENYCRNPDN 60
 DB 1 VLSCKTGNGKNYRGTMKTKNGITTCQKWSSTSPHRPSPATPSGLBENYCRNPDN 60
 QY 61 DPGFWCTTDPKRYDYCDILECEBECMHCSGENYDKISKTMGSLBQAMDSOPH 120
 DB 61 DPGFWCTTDPKRYDYCDILECEBECMHCSGENYDKISKTMGSLBQAMDSOPH 120
 QY 121 GIYPSKFPNNKLNKKNYCNPDRELPMWCFPTDPNKRWELCDIPRCTPPSSGPTYQCL 180
 DB 121 GIYPSKFPNNKLNKKNYCNPDRELPMWCFPTDPNKRWELCDIPRCTPPSSGPTYQCL 180
 QY 181 GTGENYRGNVAVTYSGHTCOHWSAQTPTHRTPTNPFCCKNLDENYCRNPDKRAPWCHT 240
 DB 181 GTGENYRGNVAVTYSGHTCOHWSAQTPTHRTPTNPFCCKNLDENYCRNPDKRAPWCHT 240
 QY 241 TNSQVMEYCKIPSCDSSPV 260
 DB 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 5

US-09-335-325-3
 ; Sequence 3, Application US/09335325
 ; Patent No. US20020164717A1
 ; GENERAL INFORMATION:

APPLICANT: Folkman, M. Judah
 O'Reilly, Michael

Cao, Yihai

Sim, B. Kim Lee

TITLE OF INVENTION: Angiostatin Fragments and Method of Use

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones & Askew

STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta

STATE: Georgia

COUNTRY: U.S.

ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/335,325

FILING DATE: 17-Jun-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/612,788

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Warren, William L.

REGISTRATION NUMBER: 36,714

REFERENCE/DOCKET NUMBER: 05213-0126

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-818-3700

TELEFAX: 404-818-3799

SEQUENCE CHARACTERISTICS:

; LENGTH: 339 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; IMMEDIATE SOURCE:
 ; CLONE: Angiostatin fragment
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-335-325-3
 Query Match 99.7%; Score 1535; DB 3; Length 339;
 Best Local Similarity 99.6%; Pred. No. 7.4e-120;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSCKTGNGKNYRGTMKTKNGITTCQKWSSTSPHRPSPATPSGLBENYCRNPDN 60
 DB 1 VLSCKTGNGKNYRGTMKTKNGITTCQKWSSTSPHRPSPATPSGLBENYCRNPDN 60
 QY 61 DPGFWCTTDPKRYDYCDILECEBECMHCSGENYDKISKTMGSLBQAMDSOPH 120
 DB 61 DPGFWCTTDPKRYDYCDILECEBECMHCSGENYDKISKTMGSLBQAMDSOPH 120
 QY 121 GIYPSKFPNNKLNKKNYCNPDRELPMWCFPTDPNKRWELCDIPRCTPPSSGPTYQCL 180
 DB 121 GIYPSKFPNNKLNKKNYCNPDRELPMWCFPTDPNKRWELCDIPRCTPPSSGPTYQCL 180
 QY 181 GTGENYRGNVAVTYSGHTCOHWSAQTPTHRTPTNPFCCKNLDENYCRNPDKRAPWCHT 240
 DB 181 GTGENYRGNVAVTYSGHTCOHWSAQTPTHRTPTNPFCCKNLDENYCRNPDKRAPWCHT 240
 QY 241 TNSQVMEYCKIPSCDSSPV 260
 DB 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 6

US-10-131-241-3
 ; Sequence 3, Application US/10131241
 ; Publication No. US20030012792A1
 ; GENERAL INFORMATION:

APPLICANT: Holaday, John W.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

FILE REFERENCE: 05213-0344 43170-271565

CURRENT FILING DATE: 2002-07-22

PRIOR FILING DATE: 1999-10-06

PRIOR APPLICATION NUMBER: US 09/413,049

PRIOR FILING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: US 60/086,586

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 339

TYPE: PRT

ORGANISM: Homo sapiens

US-10-131-241-3

Query Match 99.7%; Score 1535; DB 4; Length 339;
 Best Local Similarity 99.6%; Pred. No. 7.4e-120;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSCKTGNGKNYRGTMKTKNGITTCQKWSSTSPHRPSPATPSGLBENYCRNPDN 60
 DB 1 VLSCKTGNGKNYRGTMKTKNGITTCQKWSSTSPHRPSPATPSGLBENYCRNPDN 60

Db 1 VLSBCKTGNGKNGYGTMSKTNGITCOQMSSTSPHPRFSPATHPSBGLSENYCRNPDN 60
 QY 61 DPGWCCTTDPBKRKYDCDILCEBECMHCSENYDCKISKTMSGLECOAMDOSPHAH 120
 Db 61 DPGWCCTTDPBKRKYDCDILCEBECMHCSENYDCKISKTMSGLECOAMDOSPHAH 120
 QY 121 GYIPSKFPNKNLKKNYCRNPDRBLRPMCFCTTDPNKRWEICDI PRCTTTPSSGPTYQCLK 180
 Db 121 GYIPSKFPNKNLKKNYCRNPDRBLRPMCFCTTDPNKRWEICDI PRCTTTPSSGPTYQCLK 180
 QY 181 GTGENYRGNAVAVTSGHTCOHMSAOTPHTHRTPEPNFCKNLDENYCRNPDGKAPMCHT 240
 Db 181 GTGENYRGNAVAVTSGHTCOHMSAOTPHTHRTPEPNFCKNLDENYCRNPDGKAPMCHT 240
 QY 241 TNSQVMEYCKIIPSCDSSPV 260
 Db 241 TNSQVMEYCKIIPSCDSSPV 260

RESULT 7

US-10-127-066-3
 ; Sequence 3, Application US/10127066
 ; Publication No. US20030064926A1
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Reilly, Michael S.
 ; APPLICANT: Folkman, M. Judah
 ; APPLICANT: Cao, Yihai
 ; APPLICANT: Sim, Kim Lee
 ; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 ; FILE REFERENCE: 05213-0612 43170-272529
 ; CURRENT APPLICATION NUMBER: US/10/127,066
 ; CURRENT FILING DATE: 2002-07-23
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 339
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-127-066-3

Query Match 99.7%; Score 1535; DB 4; Length 339;
 Best Local Similarity 99.6%; Pred. No. 7.4e-120;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSBCKTGNGKNGYGTMSKTNGITCOQMSSTSPHPRFSPATHPSBGLSENYCRNPDN 60
 Db 1 VLSBCKTGNGKNGYGTMSKTNGITCOQMSSTSPHPRFSPATHPSBGLSENYCRNPDN 60
 QY 61 DPGWCCTTDPBKRKYDCDILCEBECMHCSENYDCKISKTMSGLECOAMDOSPHAH 120
 Db 61 DPGWCCTTDPBKRKYDCDILCEBECMHCSENYDCKISKTMSGLECOAMDOSPHAH 120
 QY 121 GYIPSKFPNKNLKKNYCRNPDRBLRPMCFCTTDPNKRWEICDI PRCTTTPSSGPTYQCLK 180
 Db 121 GYIPSKFPNKNLKKNYCRNPDRBLRPMCFCTTDPNKRWEICDI PRCTTTPSSGPTYQCLK 180
 QY 181 GTGENYRGNAVAVTSGHTCOHMSAOTPHTHRTPEPNFCKNLDENYCRNPDGKAPMCHT 240
 Db 181 GTGENYRGNAVAVTSGHTCOHMSAOTPHTHRTPEPNFCKNLDENYCRNPDGKAPMCHT 240
 QY 241 TNSQVMEYCKIIPSCDSSPV 260
 Db 241 TNSQVMEYCKIIPSCDSSPV 260

RESULT 8

US-10-402-364-3
 ; Sequence 3, Application US/10402364
 ; Publication No. US20040002459A1
 ; GENERAL INFORMATION:
 ; APPLICANT: O'Reilly, Michael
 ; APPLICANT: Folkman, M. Judah
 ; TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen

FILE REFERENCE: 05213-2151 (43170-252068)
 ; CURRENT APPLICATION NUMBER: US/10/402,364
 ; CURRENT FILING DATE: 2003-03-28
 ; PRIOR APPLICATION NUMBER: US/09/761,120A
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: 09/309,821
 ; PRIOR FILING DATE: 1999-05-11
 ; PRIOR APPLICATION NUMBER: 08/866,735
 ; PRIOR FILING DATE: 1997-05-30
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 339
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-402-364-3

Query Match 99.7%; Score 1535; DB 4; Length 339;
 Best Local Similarity 99.6%; Pred. No. 7.4e-120;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSBCKTGNGKNGYGTMSKTNGITCOQMSSTSPHPRFSPATHPSBGLSENYCRNPDN 60
 Db 1 VLSBCKTGNGKNGYGTMSKTNGITCOQMSSTSPHPRFSPATHPSBGLSENYCRNPDN 60
 QY 61 DPGWCCTTDPBKRKYDCDILCEBECMHCSENYDCKISKTMSGLECOAMDOSPHAH 120
 Db 61 DPGWCCTTDPBKRKYDCDILCEBECMHCSENYDCKISKTMSGLECOAMDOSPHAH 120
 QY 121 GYIPSKFPNKNLKKNYCRNPDRBLRPMCFCTTDPNKRWEICDI PRCTTTPSSGPTYQCLK 180
 Db 121 GYIPSKFPNKNLKKNYCRNPDRBLRPMCFCTTDPNKRWEICDI PRCTTTPSSGPTYQCLK 180
 QY 181 GTGENYRGNAVAVTSGHTCOHMSAOTPHTHRTPEPNFCKNLDENYCRNPDGKAPMCHT 240
 Db 181 GTGENYRGNAVAVTSGHTCOHMSAOTPHTHRTPEPNFCKNLDENYCRNPDGKAPMCHT 240
 QY 241 TNSQVMEYCKIIPSCDSSPV 260
 Db 241 TNSQVMEYCKIIPSCDSSPV 260

RESULT 9

US-10-401-108-3
 ; Sequence 3, Application US/10401108
 ; Publication No. US20040023877A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah
 ; APPLICANT: O'Reilly, Michael
 ; TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ADDRESS: Jones & Askew, LLP
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/401,108
 FILING DATE: 27-Mar-2003
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/866,735
 FILING DATE: 30-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714

REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-401-108-3

Query Match 99.7%; Score 1535; DB 4; Length 339;
Best Local Similarity 99.6%; Pred. No. 7.4e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYGTGMSKTNGITCOKWSSTSPHRRPSPATHPSEGLSENYCNPND 60
DB 1 VYLSECKTGNGKNYGTGMSKTNGITCOKWSSTSPHRRPSPATHPSEGLSENYCNPND 60
QY 61 DPGPWCYTTTDEPKRYDCDILECEBECMHCSENGYDGIKSTMSGLECOANDSOPH 120
DB 61 DPGPWCYTTTDEPKRYDCDILECEBECMHCSENGYDGIKSTMSGLECOANDSOPH 120
QY 121 GYIPSKFPKNLKNYCNRPDLRLPWCCTTDPNKRWEICDIPRCTPPSSGPTYQCL 180
DB 121 GYIPSKFPKNLKNYCNRPDLRLPWCCTTDPNKRWEICDIPRCTPPSSGPTYQCL 180
QY 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHHTERTPENFPCKNDENYCRNPDGRAPWCH 240
DB 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHHTERTPENFPCKNDENYCRNPDGRAPWCH 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 10
US-10-292-418-11
Sequence 11, Application US/10292418
Publication No. US20030139365A1
GENERAL INFORMATION:
APPLICANT: Lo, Kin-Ming
APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
FILE REFERENCE: Lex-006C1
CURRENT APPLICATION NUMBER: US/10/292,418
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/383,315
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 60/097,883
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 363
TYPE: PRT
ORGANISM: Homo sapiens
US-10-292-418-11

Query Match 99.7%; Score 1535; DB 4; Length 363;
Best Local Similarity 99.6%; Pred. No. 8e-120;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNYGTGMSKTNGITCOKWSSTSPHRRPSPATHPSEGLSENYCNPND 60
DB 2 VYLSECKTGNGKNYGTGMSKTNGITCOKWSSTSPHRRPSPATHPSEGLSENYCNPND 61
QY 61 DPGPWCYTTTDEPKRYDCDILECEBECMHCSENGYDGIKSTMSGLECOANDSOPH 120
DB 62 DPGPWCYTTTDEPKRYDCDILECEBECMHCSENGYDGIKSTMSGLECOANDSOPH 121
QY 121 GYIPSKFPKNLKNYCNRPDLRLPWCCTTDPNKRWEICDIPRCTPPSSGPTYQCL 180
DB 122 GYIPSKFPKNLKNYCNRPDLRLPWCCTTDPNKRWEICDIPRCTPPSSGPTYQCL 181
QY 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHHTERTPENFPCKNDENYCRNPDGRAPWCH 240
DB 182 GTGENYRGNAVAVTSGHTCOHWSAOTPHHTERTPENFPCKNDENYCRNPDGRAPWCH 241
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 242 TNSQVRWEYCKIPSCDSSPV 261

RESULT 11
US-09-873-676-1
Sequence 1, Application US/09873676
Patent No. US20020077289A1
GENERAL INFORMATION:
APPLICANT: Macdonald, Nicholas J.
APPLICANT: Sim, Kim L.
TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
FILE REFERENCE: 05213-0378 (43170-259333)
CURRENT APPLICATION NUMBER: US/09/873,676
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: US 60/209,065
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/289,387
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-09-873-676-1

Query Match 99.7%; Score 1535; DB 3; Length 378;
Best Local Similarity 99.6%; Pred. No. 8.4e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYGTGMSKTNGITCOKWSSTSPHRRPSPATHPSEGLSENYCNPND 60
DB 6 VYLSECKTGNGKNYGTGMSKTNGITCOKWSSTSPHRRPSPATHPSEGLSENYCNPND 65
QY 61 DPGPWCYTTTDEPKRYDCDILECEBECMHCSENGYDGIKSTMSGLECOANDSOPH 120
DB 66 DPGPWCYTTTDEPKRYDCDILECEBECMHCSENGYDGIKSTMSGLECOANDSOPH 125
QY 121 GYIPSKFPKNLKNYCNRPDLRLPWCCTTDPNKRWEICDIPRCTPPSSGPTYQCL 180
DB 126 GYIPSKFPKNLKNYCNRPDLRLPWCCTTDPNKRWEICDIPRCTPPSSGPTYQCL 185
QY 181 GTGENYRGNAVAVTSGHTCOHWSAOTPHHTERTPENFPCKNDENYCRNPDGRAPWCH 240
DB 186 GTGENYRGNAVAVTSGHTCOHWSAOTPHHTERTPENFPCKNDENYCRNPDGRAPWCH 245
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 246 TNSQVRWEYCKIPSCDSSPV 265

RESULT 12
US-09-335-325-42

ORGANISM: Homo sapiens
US-10-127-066-42

Query Match 99.7%; Score 1535; DB 4; Length 378;
Best Local Similarity 99.6%; Pred. No. 8.4e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VILSECKTGNGKRYGTMTKNGITCQKMSSTSPHRPSPATHPSEGLSENYCRNPDN 60
DB 6 VILSECKTGNGKRYGTMTKNGITCQKMSSTSPHRPSPATHPSEGLSENYCRNPDN 65
QY 61 DQGFMCYTTDEPKRYDYCDILECEBECNHGSENYDGKISKTMGSLGCQAWDSQSPH 120
DB 66 DQGFMCYTTDEPKRYDYCDILECEBECNHGSENYDGKISKTMGSLGCQAWDSQSPH 125
QY 121 GIIPSKFPKKNLKKNYCRNPDRELPRWCCTTDPNKNMELCDIPRCTPPSSGPTYQCLK 180
DB 126 GIIPSKFPKKNLKKNYCRNPDRELPRWCCTTDPNKNMELCDIPRCTPPSSGPTYQCLK 185
QY 181 GTGENYRGNAVTVSGHTCQHMSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 240
DB 186 GTGENYRGNAVTVSGHTCQHMSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 245
QY 241 TNSQVRMEYCKIPSCDSSPV 260
DB 246 TNSQVRMEYCKIPSCDSSPV 265

RESULT 15

US-10-304-287-7
; Sequence 7, Application US/10304287
; Publication No. US20030083234A1
; GENERAL INFORMATION:
; APPLICANT: Waisman, David M.
; APPLICANT: Kwon, Mijung
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
; FILE REFERENCE: ME02-001
; CURRENT APPLICATION NUMBER: US/10/304,287
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 60/333,866
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Word
; SEQ ID NO 7
; LENGTH: 391
; TYPE: PRT
; ORGANISM: mammalian
US-10-304-287-7

Query Match 99.7%; Score 1535; DB 4; Length 391;
Best Local Similarity 99.6%; Pred. No. 8.7e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VILSECKTGNGKRYGTMTKNGITCQKMSSTSPHRPSPATHPSEGLSENYCRNPDN 60
DB 2 VILSECKTGNGKRYGTMTKNGITCQKMSSTSPHRPSPATHPSEGLSENYCRNPDN 61
QY 61 DQGFMCYTTDEPKRYDYCDILECEBECNHGSENYDGKISKTMGSLGCQAWDSQSPH 120
DB 62 DQGFMCYTTDEPKRYDYCDILECEBECNHGSENYDGKISKTMGSLGCQAWDSQSPH 121
QY 121 GIIPSKFPKKNLKKNYCRNPDRELPRWCCTTDPNKNMELCDIPRCTPPSSGPTYQCLK 180
DB 122 GIIPSKFPKKNLKKNYCRNPDRELPRWCCTTDPNKNMELCDIPRCTPPSSGPTYQCLK 181
QY 181 GTGENYRGNAVTVSGHTCQHMSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 240
DB 182 GTGENYRGNAVTVSGHTCQHMSAOTPHHTERTPENPCKNLDENYCRNPDGRAPWCHT 241
QY 241 TNSQVRMEYCKIPSCDSSPV 260
DB 242 TNSQVRMEYCKIPSCDSSPV 261

Search completed: January 25, 2006, 17:21:52
Job time : 118 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2006, 17:04:06 ; Search time 45 Seconds
(without alignments)
477.682 Million cell updates/sec

Title: US-09-502-176-2
Perfect score: 1540
Sequence: 1 VYLSECKTGNGKNRYGTWSK.....TNSQVREYCKIPSCDSFV 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--|
| 1 | 1540 | 100.0 | 260 | 2 | US-09-982-516-1 Sequence 1, Appli |
| 2 | 1535 | 99.7 | 339 | 1 | US-08-248-629A-3 Sequence 3, Appli |
| 3 | 1535 | 99.7 | 339 | 1 | US-08-451-932-3 Sequence 3, Appli |
| 4 | 1535 | 99.7 | 339 | 1 | US-08-452-260-3 Sequence 3, Appli |
| 5 | 1535 | 99.7 | 339 | 1 | US-08-326-788-3 Sequence 3, Appli |
| 6 | 1535 | 99.7 | 339 | 1 | US-08-612-788-3 Sequence 3, Appli |
| 7 | 1535 | 99.7 | 339 | 1 | US-08-605-598B-3 Sequence 3, Appli |
| 8 | 1535 | 99.7 | 339 | 1 | US-08-429-743-3 Sequence 3, Appli |
| 9 | 1535 | 99.7 | 339 | 1 | US-08-866-735-3 Sequence 3, Appli |
| 10 | 1535 | 99.7 | 339 | 2 | US-09-066-028-3 Sequence 3, Appli |
| 11 | 1535 | 99.7 | 339 | 2 | US-09-335-325-3 Sequence 3, Appli |
| 12 | 1535 | 99.7 | 339 | 4 | US-09-335-614-3 Sequence 3, Appli |
| 13 | 1535 | 99.7 | 339 | 4 | PCR-US95-05107-3 Sequence 3, Appli |
| 14 | 1535 | 99.7 | 374 | 2 | US-09-377-250-3 Sequence 3, Appli |
| 15 | 1535 | 99.7 | 375 | 2 | US-09-377-250-2 Sequence 2, Appli |
| 16 | 1535 | 99.7 | 378 | 1 | US-08-612-788-42 Sequence 42, Appli |
| 17 | 1535 | 99.7 | 378 | 2 | US-09-066-028-42 Sequence 42, Appli |
| 18 | 1535 | 99.7 | 378 | 2 | US-09-206-059-1 Sequence 1, Appli |
| 19 | 1535 | 99.7 | 378 | 2 | US-09-335-325-42 Sequence 42, Appli |
| 20 | 1535 | 99.7 | 378 | 2 | US-09-335-614-42 Sequence 42, Appli |
| 21 | 1535 | 99.7 | 451 | 2 | US-09-377-250-1 Sequence 1, Appli |
| 22 | 1535 | 99.7 | 452 | 2 | US-09-377-250-4 Sequence 4, Appli |
| 23 | 1535 | 99.7 | 790 | 1 | US-08-469-486-54 Sequence 54, Appli |
| 24 | 1535 | 99.7 | 790 | 1 | US-08-469-656-54 Sequence 54, Appli |
| 25 | 1535 | 99.7 | 791 | 1 | US-08-643-219-1 Sequence 1, Appli |
| 26 | 1535 | 99.7 | 791 | 1 | US-09-131-995-1 Sequence 1, Appli |
| 27 | 1535 | 99.7 | 791 | 1 | US-08-832-087B-1 Sequence 1, Appli |

| | | | | | |
|----|------|------|-----|---|---|
| 28 | 1535 | 99.7 | 791 | 2 | US-08-851-350-1 Sequence 1, Appli |
| 29 | 1535 | 99.7 | 791 | 2 | US-09-132-154-1 Sequence 1, Appli |
| 30 | 1535 | 99.7 | 791 | 2 | US-08-991-761A-6 Sequence 6, Appli |
| 31 | 1535 | 99.7 | 791 | 2 | US-08-924-287A-1 Sequence 1, Appli |
| 32 | 1535 | 99.7 | 791 | 2 | US-10-360-101-257 Sequence 257, App |
| 33 | 1535 | 99.7 | 810 | 1 | US-07-854-603-2 Sequence 2, Appli |
| 34 | 1535 | 99.7 | 810 | 1 | US-08-147-000B-29 Sequence 29, Appli |
| 35 | 1535 | 99.7 | 810 | 2 | US-09-086-514-1 Sequence 1, Appli |
| 36 | 1535 | 99.7 | 810 | 2 | US-09-192-012-5 Sequence 5, Appli |
| 37 | 1535 | 99.7 | 810 | 2 | US-09-403-736-1 Sequence 1, Appli |
| 38 | 1535 | 99.7 | 810 | 2 | US-09-701-265-1 Sequence 1, Appli |
| 39 | 1535 | 99.7 | 814 | 1 | US-08-750-711-1 Sequence 1, Appli |
| 40 | 1532 | 99.5 | 713 | 2 | US-09-949-016-9983 Sequence 9983, Ap |
| 41 | 1531 | 99.4 | 369 | 2 | US-09-701-265-2 Sequence 2, Appli |
| 42 | 1531 | 99.4 | 810 | 6 | 5200340-8 Patent No. 5200340 |
| 43 | 1511 | 98.1 | 352 | 1 | US-08-612-788-40 Sequence 40, Appli |
| 44 | 1511 | 98.1 | 352 | 2 | US-09-066-028-40 Sequence 40, Appli |
| 45 | 1511 | 98.1 | 352 | 2 | US-09-335-325-40 Sequence 40, Appli |

ALIGNMENTS

```
RESULT 1
US-09-982-516-1
; Sequence 1, Application US/09982516
; Patent No. 6723536
; GENERAL INFORMATION:
; APPLICANT: Madsen, John
; APPLICANT: Liang, Hong
; APPLICANT: Sim, Kim Lee
; APPLICANT: Zhou, Xinhua
; APPLICANT: Chang-Murad, Amy
; APPLICANT: Boerner, Renee J.
; APPLICANT: Bernerjo, Lourdes L.
; APPLICANT: Mistry, Jitroz R.
; APPLICANT: Schrimsher, Jeffrey L.
; APPLICANT: Shepard, Scott R.
; TITLE OF INVENTION: Method of Producing and Purifying Angiotensin Protein
; FILE REFERENCE: 05213-0562 43170-264313
; CURRENT APPLICATION NUMBER: US/09/982,516
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/32843
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US 60/168,919
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-982-516-1

Query Match          100.0%; Score 1540; DB 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 3.3e-139;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNRYGTWSKTTGKNGITTCQKMSSTSPHRRFSPATHPSEGLEENYCRNDN 60
DB 1 VYLSECKTGNGKNRYGTWSKTTGKNGITTCQKMSSTSPHRRFSPATHPSEGLEENYCRNDN 60

QY 61 DPGPMCTTDPKRYDYCDILCEBEGCMHSGENYDGKISKTSGLCQAMDSQSPRAH 120
DB 61 DPGPMCTTDPKRYDYCDILCEBEGCMHSGENYDGKISKTSGLCQAMDSQSPRAH 120

QY 121 GYISKFPNKULKKYKCNPNRRLRPMCFCTTDPNKNRMLCDIIPCTTTPSSGPTYOCLK 180
DB 121 GYISKFPNKULKKYKCNPNRRLRPMCFCTTDPNKNRMLCDIIPCTTTPSSGPTYOCLK 180

QY 181 GTGENYRGNVAVTYSGHTCQMSAQTPHTHRTENPFCCKNLDENYCNPDGKAPWCHT 240
DB 181 GTGENYRGNVAVTYSGHTCQMSAQTPHTHRTENPFCCKNLDENYCNPDGKAPWCHT 240
```

OY 241 TNSOVRWEYCKIPSCDSSPV 260
 DB 241 TNSOVRWEYCKIPSCDSSPV 260

RESULT 2

US-08-248-629A-3
 ; Sequence 3, Application US/08248629A
 ; Patent No. 5639725

GENERAL INFORMATION:

APPLICANT: Folkman, Judah
 APPLICANT: O'Reilly, Michael
 TITLE OF INVENTION: Angiostatin and Method of Use
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50
 COMPUTER: Macintosh
 OPERATING SYSTEM: 7.0
 SOFTWARE: Microsoft Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248,629A
 FILING DATE: 04/26/94
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Larry W. Scults, Ph.D.
 REGISTRATION NUMBER: 34,025
 REFERENCE/DOCKET NUMBER: 05213-0120
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 339
 TYPE: amino acid
 TOPOLOGY: linear

US-08-248-629A-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.4e-138;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VYLSECKTNGKNGKNGTMSKTKNGITCOKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60
 DB 1 VYLSECKTNGKNGKNGTMSKTKNGITCOKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60
 OY 61 DPQGPWCYTTDPKRYDYCDILCEBECMHGSGENYDGIKSTMSGLSCQAWDSOSPHAH 120
 DB 61 DPQGPWCYTTDPKRYDYCDILCEBECMHGSGENYDGIKSTMSGLSCQAWDSOSPHAH 120
 OY 121 GYIPSPFNKLNKKYCNRPDRELAPWCFTTDPNKGWELCDIPRCTPPPSGPTTQCLK 180
 DB 121 GYIPSPFNKLNKKYCNRPDRELAPWCFTTDPNKGWELCDIPRCTPPPSGPTTQCLK 180
 OY 181 GTGENYRGNAVAVTVSGHTCOHWSAQTPHTERTPENPCKNIDENYCRNPDGKRAPWCHT 240
 DB 181 GTGENYRGNAVAVTVSGHTCOHWSAQTPHTERTPENPCKNIDENYCRNPDGKRAPWCHT 240
 OY 241 TNSOVRWEYCKIPSCDSSPV 260
 DB 241 TNSOVRWEYCKIPSCDSSPV 260

RESULT 3

US-08-451-932-3
 ; Sequence 3, Application US/08451932
 ; Patent No. 5733876

GENERAL INFORMATION:

APPLICANT: Folkman, Judah
 APPLICANT: O'Reilly, Michael
 TITLE OF INVENTION: Method of Treating an Angiogenic
 TITLE OF INVENTION: Disease
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50
 COMPUTER: Macintosh
 OPERATING SYSTEM: 7.0
 SOFTWARE: Microsoft Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/451,932
 FILING DATE: 05/26/95
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/248,629
 FILING DATE: 04/26/94
 ATTORNEY/AGENT INFORMATION:
 NAME: Larry W. Scults, Ph.D.
 REGISTRATION NUMBER: 34,025
 REFERENCE/DOCKET NUMBER: 05213-0123
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 339
 TYPE: amino acid
 TOPOLOGY: linear

US-08-451-932-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.4e-138;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VYLSECKTNGKNGKNGTMSKTKNGITCOKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60
 DB 1 VYLSECKTNGKNGKNGTMSKTKNGITCOKWSSTSPHPRPSPATHPSEGLEENYCRNPDN 60
 OY 61 DPQGPWCYTTDPKRYDYCDILCEBECMHGSGENYDGIKSTMSGLSCQAWDSOSPHAH 120
 DB 61 DPQGPWCYTTDPKRYDYCDILCEBECMHGSGENYDGIKSTMSGLSCQAWDSOSPHAH 120
 OY 121 GYIPSPFNKLNKKYCNRPDRELAPWCFTTDPNKGWELCDIPRCTPPPSGPTTQCLK 180
 DB 121 GYIPSPFNKLNKKYCNRPDRELAPWCFTTDPNKGWELCDIPRCTPPPSGPTTQCLK 180
 OY 181 GTGENYRGNAVAVTVSGHTCOHWSAQTPHTERTPENPCKNIDENYCRNPDGKRAPWCHT 240
 DB 181 GTGENYRGNAVAVTVSGHTCOHWSAQTPHTERTPENPCKNIDENYCRNPDGKRAPWCHT 240
 OY 241 TNSOVRWEYCKIPSCDSSPV 260
 DB 241 TNSOVRWEYCKIPSCDSSPV 260

RESULT 4

US-08-452-260-3
 ; Sequence 3, Application US/08452260
 ; Patent No. 5776704

GENERAL INFORMATION:

```
/ APPLICANT: Folkman, Judah
/ APPLICANT: O'Reilly, Michael
/ TITLE OF INVENTION: Method of Diagnosing an Angiogenic
/ TITLE OF INVENTION: Disease
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Jones & Askew
/ STREET: 191 Peachtree Street, 37th Floor
/ CITY: Atlanta
/ STATE: Georgia
/ COUNTRY: USA
/ ZIP: 30303-1769
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50
/ COMPUTER: Macintosh
/ OPERATING SYSTEM: 7.0
/ SOFTWARE: Microsoft Word
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/452,260
/ FILING DATE: 05/26/95
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/248,629
/ FILING DATE: 04/26/94
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Larry W. Stults, Ph.D.
/ REGISTRATION NUMBER: 34,025
/ REFERENCE/DOCKET NUMBER: 05213-0124
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 404-818-3700
/ TELEFAX: 404-818-3799
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 339
/ TYPE: amino acid
/ TOPOLOGY: linear
/
US-08-452-260-3

Query Match          99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSSECTGNGKNYGTMSKTNGITCOKMSSTSPHRPSPATPSEGLSENYCNPN 60
DB 1 VLSSECTGNGKNYGTMSKTNGITCOKMSSTSPHRPSPATPSEGLSENYCNPN 60
QY 61 DPGPWCYTTDEPKRYDYCDILECEBECMHGSGENYDGKISKTMGLBQAMDSPH 120
DB 61 DPGPWCYTTDEPKRYDYCDILECEBECMHGSGENYDGKISKTMGLBQAMDSPH 120
QY 121 GYIPSKFPKNLKKNYCRNPDLRPMWCTTDPNKRWEICDIPRCTPPSSGPTYQCK 180
DB 121 GYIPSKFPKNLKKNYCRNPDLRPMWCTTDPNKRWEICDIPRCTPPSSGPTYQCK 180
QY 181 GGENYRGNVAVTYSGHCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GGENYRGNVAVTYSGHCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 5
US-08-326-785-3
/ Sequence 3, Application US/08326785
/ Patent No. 5792845
/ GENERAL INFORMATION:
/ APPLICANT: Folkman, Judah
/ APPLICANT: O'Reilly, Michael
/ TITLE OF INVENTION: Angiostatin and Method of Use
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
```

```
/ ADDRESSEE: Jones & Askew
/ STREET: 191 Peachtree Street, 37th Floor
/ CITY: Atlanta
/ STATE: Georgia
/ COUNTRY: USA
/ ZIP: 30303-1769
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50
/ COMPUTER: Macintosh
/ OPERATING SYSTEM: 7.0
/ SOFTWARE: Microsoft Word
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/326,785
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/248,629
/ FILING DATE: 04/26/94
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Larry W. Stults, Ph.D.
/ REGISTRATION NUMBER: 34,025
/ REFERENCE/DOCKET NUMBER: 05213-0121
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 404-818-3700
/ TELEFAX: 404-818-3799
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 339
/ TYPE: amino acid
/ TOPOLOGY: linear
/
US-08-326-785-3
```

```
Query Match          99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSSECTGNGKNYGTMSKTNGITCOKMSSTSPHRPSPATPSEGLSENYCNPN 60
DB 1 VLSSECTGNGKNYGTMSKTNGITCOKMSSTSPHRPSPATPSEGLSENYCNPN 60
QY 61 DPGPWCYTTDEPKRYDYCDILECEBECMHGSGENYDGKISKTMGLBQAMDSPH 120
DB 61 DPGPWCYTTDEPKRYDYCDILECEBECMHGSGENYDGKISKTMGLBQAMDSPH 120
QY 121 GYIPSKFPKNLKKNYCRNPDLRPMWCTTDPNKRWEICDIPRCTPPSSGPTYQCK 180
DB 121 GYIPSKFPKNLKKNYCRNPDLRPMWCTTDPNKRWEICDIPRCTPPSSGPTYQCK 180
QY 181 GGENYRGNVAVTYSGHCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GGENYRGNVAVTYSGHCOHWSAOTPHHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 6
US-08-612-788-3
/ Sequence 3, Application US/08612788
/ Patent No. 5837682
/ GENERAL INFORMATION:
/ APPLICANT: Folkman, M. Judah
/ APPLICANT: O'Reilly, Michael
/ APPLICANT: Cao, Yihai
/ APPLICANT: Sim, B. Kim Lee
/ TITLE OF INVENTION: Angiostatin Fragments and Method of Use
/ NUMBER OF SEQUENCES: 45
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Jones & Askew
/ STREET: 191 Peachtree Street, 37th Floor
/ CITY: Atlanta
/ STATE: Georgia
```

COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
US-08-612-788-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRRFPSPATPSGEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRRFPSPATPSGEGLEENYCRNPDN 60
QY 61 DPGPCWCTTDPPEKRYDYCDILECEBECMHCSGENYDGIKISKTMSGLGCOAWDSQSPH 120
DB 61 DPGPCWCTTDPPEKRYDYCDILECEBECMHCSGENYDGIKISKTMSGLGCOAWDSQSPH 120
QY 121 GYIPSKFPKNLKNKYCRNPDELRPWCFTTDPNKRWEICDIIPRCTTTPPSGPTTYOCLK 180
DB 121 GYIPSKFPKNLKNKYCRNPDELRPWCFTTDPNKRWEICDIIPRCTTTPPSGPTTYOCLK 180
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 7
US-08-605-598B-3
Sequence 3, Application US/08605598B
Patent No. 5863372
GENERAL INFORMATION:
APPLICANT: Folkman, M. Judah
APPLICANT: Lin, Jie
APPLICANT: O'Reilly, Michael S.
TITLE OF INVENTION: Aggregate Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta

STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,598B
FILING DATE: 22-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Human Angiostatin
US-08-605-598B-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRRFPSPATPSGEGLEENYCRNPDN 60
DB 1 VYLSECKTGNGKNYRGTMSTKNGITCQKMSSTSPHRRFPSPATPSGEGLEENYCRNPDN 60
QY 61 DPGPCWCTTDPPEKRYDYCDILECEBECMHCSGENYDGIKISKTMSGLGCOAWDSQSPH 120
DB 61 DPGPCWCTTDPPEKRYDYCDILECEBECMHCSGENYDGIKISKTMSGLGCOAWDSQSPH 120
QY 121 GYIPSKFPKNLKNKYCRNPDELRPWCFTTDPNKRWEICDIIPRCTTTPPSGPTTYOCLK 180
DB 121 GYIPSKFPKNLKNKYCRNPDELRPWCFTTDPNKRWEICDIIPRCTTTPPSGPTTYOCLK 180
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENPCKNLDENYCRNPDGKRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 8
US-08-429-743-3
Sequence 3, Application US/08429743
Patent No. 5885795
GENERAL INFORMATION:
APPLICANT: O'Reilly, Michael
APPLICANT: Folkman, M. Judah
APPLICANT: Sim, Kim Lee
APPLICANT: Cao, Yihai
TITLE OF INVENTION: Angiostatin and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769

COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,743
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,629
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/326,785
FILING DATE: 20-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, James D.
REGISTRATION NUMBER: 31,771
REFERENCE/DOCKET NUMBER: 05213-0122
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-429-743-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSLCKTGNGKNYGTMSKTNKGTTCQKWSSTSPHRRPSPATPSBGLBENYCNPN 60
DB 1 VLSLCKTGNGKNYGTMSKTNKGTTCQKWSSTSPHRRPSPATPSBGLBENYCNPN 60
QY 61 DPGPWCYTTTDEPKRYDCDILECEBECMHGSENYDGKISKTMGLGCOAWDSOPH 120
DB 61 DPGPWCYTTTDEPKRYDCDILECEBECMHGSENYDGKISKTMGLGCOAWDSOPH 120
QY 121 GYIPKFPKNLKNYCNRPDLRPWCFTTDPNKRMBELCDIPRCTPPSSGPTYQCL 180
DB 121 GYIPKFPKNLKNYCNRPDLRPWCFTTDPNKRMBELCDIPRCTPPSSGPTYQCL 180
QY 181 GTGENYRGNAVTVSGHTCOHWSAOTPHTHRTPENFPCKNDENYCNRPDGRAPWCHT 240
DB 181 GTGENYRGNAVTVSGHTCOHWSAOTPHTHRTPENFPCKNDENYCNRPDGRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSPV 260
DB 241 TNSQVRWEYCKIPSCDSPV 260

RESULT 9
US-08-866-735-3
Sequence 3, Application US/08866735
Patent No. 5945403
GENERAL INFORMATION:
APPLICANT: Folkmann, M. Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia

COUNTRY: USA
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,735
FILING DATE: 30-MAY-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05940-0129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiostatin fragment
US-08-866-735-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSLCKTGNGKNYGTMSKTNKGTTCQKWSSTSPHRRPSPATPSBGLBENYCNPN 60
DB 1 VLSLCKTGNGKNYGTMSKTNKGTTCQKWSSTSPHRRPSPATPSBGLBENYCNPN 60
QY 61 DPGPWCYTTTDEPKRYDCDILECEBECMHGSENYDGKISKTMGLGCOAWDSOPH 120
DB 61 DPGPWCYTTTDEPKRYDCDILECEBECMHGSENYDGKISKTMGLGCOAWDSOPH 120
QY 121 GYIPKFPKNLKNYCNRPDLRPWCFTTDPNKRMBELCDIPRCTPPSSGPTYQCL 180
DB 121 GYIPKFPKNLKNYCNRPDLRPWCFTTDPNKRMBELCDIPRCTPPSSGPTYQCL 180
QY 181 GTGENYRGNAVTVSGHTCOHWSAOTPHTHRTPENFPCKNDENYCNRPDGRAPWCHT 240
DB 181 GTGENYRGNAVTVSGHTCOHWSAOTPHTHRTPENFPCKNDENYCNRPDGRAPWCHT 240
QY 241 TNSQVRWEYCKIPSCDSPV 260
DB 241 TNSQVRWEYCKIPSCDSPV 260

RESULT 10
US-09-066-028-3
Sequence 3, Application US/09066028
Patent No. 602468
GENERAL INFORMATION:
APPLICANT: Folkmann, M. Judah
APPLICANT: O'Reilly, Michael
APPLICANT: Cao, Yihai
APPLICANT: Sim, B. Kim Lee
TITLE OF INVENTION: Angiostatin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,028
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/612,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Marten, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiotensin fragment
US-09-066-028-3

Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSSECKTGNGKNYRGTMSTKNGITCOKMSSTSPHPRPSPATPSPBGLSENYCRPNPN 60
DB 1 VLSSECKTGNGKNYRGTMSTKNGITCOKMSSTSPHPRPSPATPSPBGLSENYCRPNPN 60
QY 61 DPOGPMCYTTDDPEKRYDYCDILECEBECMHGSGENTDGKISKTMGSLBQAMDSQSPHAA 120
DB 61 DPOGPMCYTTDDPEKRYDYCDILECEBECMHGSGENTDGKISKTMGSLBQAMDSQSPHAA 120
QY 121 GYIPSKFPNKNLKKNYCRNPDRRLRPMCTTDPNKMWEICDIPRCTTPPSSGPTYOCLK 180
DB 121 GYIPSKFPNKNLKKNYCRNPDRRLRPMCTTDPNKMWEICDIPRCTTPPSSGPTYOCLK 180
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLDENYCRNPDGRAPWCHT 240
DB 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLDENYCRNPDGRAPWCHT 240
QY 241 TNSQVMEYCKIPSCDSSPV 260
DB 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 11
US-09-335-325-3
; Sequence 3, Application US/09335325
; Patent No. 6521439
; GENERAL INFORMATION:
; APPLICANT: Folkman, M. Judah
; O'Reilly, Michael
; Cao, Yihai
; Sim, B. Kim Lee

TITLE OF INVENTION: Angiotensin Fragments and Method of Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Lekey
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30303-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marten, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Angiotensin fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-335-325-3

Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSSECKTGNGKNYRGTMSTKNGITCOKMSSTSPHPRPSPATPSPBGLSENYCRPNPN 60
DB 1 VLSSECKTGNGKNYRGTMSTKNGITCOKMSSTSPHPRPSPATPSPBGLSENYCRPNPN 60
QY 61 DPOGPMCYTTDDPEKRYDYCDILECEBECMHGSGENTDGKISKTMGSLBQAMDSQSPHAA 120
DB 61 DPOGPMCYTTDDPEKRYDYCDILECEBECMHGSGENTDGKISKTMGSLBQAMDSQSPHAA 120
QY 121 GYIPSKFPNKNLKKNYCRNPDRRLRPMCTTDPNKMWEICDIPRCTTPPSSGPTYOCLK 180
DB 121 GYIPSKFPNKNLKKNYCRNPDRRLRPMCTTDPNKMWEICDIPRCTTPPSSGPTYOCLK 180
QY 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLDENYCRNPDGRAPWCHT 240
DB 181 GTGENYRGNAVAVTSGHTCOHWSAQTPTHTERTPENFPCKNLDENYCRNPDGRAPWCHT 240
QY 241 TNSQVMEYCKIPSCDSSPV 260
DB 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 12
US-09-335-614-3
; Sequence 3, Application US/09335614

Db 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 14

US-09-377-250-3
 ; Sequence 3, Application US/09377250
 ; Patent No. 6365364
 ; GENERAL INFORMATION:
 ; APPLICANT: MANN, KENNETH G.
 ; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
 ; FILE REFERENCE: 48409/360
 ; CURRENT APPLICATION NUMBER: US/09/377,250
 ; CURRENT FILING DATE: 1999-08-19
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 374
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: angiogenesis inhibitor
 ; NAME/KEY: MOD RES
 ; LOCATION: (264)
 ; OTHER INFORMATION: Xaa = Gln or Glu
 US-09-377-250-3

Query Match 99.7%; Score 1535; DB 2; Length 374;
 Best Local Similarity 99.6%; Pred. No. 1.6e-138;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTNGKNGKNGTMSKTNGITCQKMSSTSPHPRFSPATHPSEGLEENYCRNPDN 60
 1 VYLSECKTNGKNGKNGTMSKTNGITCQKMSSTSPHPRFSPATHPSEGLEENYCRNPDN 60
 Db 1 VYLSECKTNGKNGKNGTMSKTNGITCQKMSSTSPHPRFSPATHPSEGLEENYCRNPDN 60
 QY 61 DPGFWCYTTDPEKRYDYCDILBCEBECMHCSEGENYDGKISKWISGLECOAMDOSPHAH 120
 61 DPGFWCYTTDPEKRYDYCDILBCEBECMHCSEGENYDGKISKWISGLECOAMDOSPHAH 120
 Db 61 DPGFWCYTTDPEKRYDYCDILBCEBECMHCSEGENYDGKISKWISGLECOAMDOSPHAH 120
 QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
 Db 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
 QY 181 GTGENYRGNAVAVTVSGHTCOHMSAQTPTHTERTPENPCNLDENYCRNPDGKRAPWCHT 240
 181 GTGENYRGNAVAVTVSGHTCOHMSAQTPTHTERTPENPCNLDENYCRNPDGKRAPWCHT 240
 Db 181 GTGENYRGNAVAVTVSGHTCOHMSAQTPTHTERTPENPCNLDENYCRNPDGKRAPWCHT 240
 QY 241 TNSQVMEYCKIPSCDSSPV 260
 241 TNSQVMEYCKIPSCDSSPV 260
 Db 241 TNSQVMEYCKIPSCDSSPV 260

RESULT 15

US-09-377-250-2
 ; Sequence 2, Application US/09377250
 ; Patent No. 6365364
 ; GENERAL INFORMATION:
 ; APPLICANT: MANN, KENNETH G.
 ; APPLICANT: SWORDS JENNY, NANCY
 ; TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF
 ; FILE REFERENCE: 48409/360
 ; CURRENT APPLICATION NUMBER: US/09/377,250
 ; CURRENT FILING DATE: 1999-08-19
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 375
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: angiogenesis inhibitor
 ; FEATURE:

; NAME/KEY: MOD RES
 ; LOCATION: (265)
 ; OTHER INFORMATION: Xaa = Gln or Glu
 US-09-377-250-2

Query Match 99.7%; Score 1535; DB 2; Length 375;
 Best Local Similarity 99.6%; Pred. No. 1.6e-138;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTNGKNGKNGTMSKTNGITCQKMSSTSPHPRFSPATHPSEGLEENYCRNPDN 60
 2 VYLSECKTNGKNGKNGTMSKTNGITCQKMSSTSPHPRFSPATHPSEGLEENYCRNPDN 61
 Db 2 VYLSECKTNGKNGKNGTMSKTNGITCQKMSSTSPHPRFSPATHPSEGLEENYCRNPDN 61
 QY 61 DPGFWCYTTDPEKRYDYCDILBCEBECMHCSEGENYDGKISKWISGLECOAMDOSPHAH 120
 62 DPGFWCYTTDPEKRYDYCDILBCEBECMHCSEGENYDGKISKWISGLECOAMDOSPHAH 121
 Db 62 DPGFWCYTTDPEKRYDYCDILBCEBECMHCSEGENYDGKISKWISGLECOAMDOSPHAH 121
 QY 121 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 180
 122 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 181
 Db 122 GYIPSKFPNKLKKNYCRNPDRELPRWCFTTDPNKRWELCDIPRCTTPPSSGPTYQCLK 181
 QY 181 GTGENYRGNAVAVTVSGHTCOHMSAQTPTHTERTPENPCNLDENYCRNPDGKRAPWCHT 240
 182 GTGENYRGNAVAVTVSGHTCOHMSAQTPTHTERTPENPCNLDENYCRNPDGKRAPWCHT 241
 Db 182 GTGENYRGNAVAVTVSGHTCOHMSAQTPTHTERTPENPCNLDENYCRNPDGKRAPWCHT 241
 QY 241 TNSQVMEYCKIPSCDSSPV 260
 242 TNSQVMEYCKIPSCDSSPV 261
 Db 242 TNSQVMEYCKIPSCDSSPV 261

Search completed: January 25, 2006, 17:11:54
 Job time : 46 secs

Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGRGTGMSKTNGITCOKMSSTSPHRPRFPATHPSEGLSENYCRNPDN 60
 DB 1 VILSECKTGNGKNGRGTGMSKTNGITCOKMSSTSPHRPRFPATHPSEGLSENYCRNPDN 60
 QY 61 DPQPMCYTTDPKRYDYCDILCEBECCHMGSGENYDKISKTMSGLECOAMDOSPHAH 120
 DB 61 DPQPMCYTTDPKRYDYCDILCEBECCHMGSGENYDKISKTMSGLECOAMDOSPHAH 120
 QY 121 GYIPSKFPNNKLNKKNYCRNPDRELAPWCFTTDPNKRWELCDI PRCTTTPSSGPTYQCLK 180
 DB 121 GYIPSKFPNNKLNKKNYCRNPDRELAPWCFTTDPNKRWELCDI PRCTTTPSSGPTYQCLK 180
 QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGRAPWCHT 240
 DB 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGRAPWCHT 240
 QY 241 TNSQVMEYCKIIPSCDSSPV 260
 DB 241 TNSQVMEYCKIIPSCDSSPV 260

RESULT 2
 AAU01209
 ID AAU01209 standard; protein; 260 AA.
 AC AAU01209;
 XX 26-SEP-2001 (first entry)
 DE Human Angiostatin (hASv3) protein.
 XX
 KW Human: Angiostatin; recombinant production; cation exchange column;
 KW fermentation; angiogenesis mediated disease; leukaemia; tumour;
 KW rheumatoid arthritis; plaque neovascularisation.
 XX
 OS Homo sapiens.
 XX
 PN MO200140260-A2.
 PD 07-JUN-2001.
 PF 04-DEC-2000; 2000MO-US032843.
 PR 03-DEC-1999; 99US-0168919P.
 XX
 PA (ENTR-) ENTREMED INC.
 XX
 PI Madesen J, Liang H, Sim KL, Zhou X, Chang-Murad A, Boerner RJ;
 PI Bermejo LL, Mistry FR, Schrimsher JL, Shepard SR;
 XX
 DR WPI; 2001-408277/43.
 DR N-PSDB; AAS04181.
 XX
 PT Purifying recombinant angiostatin, involves applying fermented broth
 PT containing angiostatin to expanded bed cation exchange column, anion
 PT exchange column, hydroxyapatite column, hydrophobic column and a
 PT membrane.
 XX
 PS Example 1; Page 22; 49p; English.
 XX
 CC The present sequence representing Angiostatin protein is given in an
 CC invention providing a method for recombinant production, recovery and
 CC purification of Angiostatin protein. Purification of recombinant
 CC Angiostatin comprises applying crude fermentation broth containing the
 CC protein to an expanded bed cation exchange column, eluting it, and
 CC applying the eluate to anion exchange column, repeating the process of
 CC eluting and applying, to hydroxyapatite column, hydrophobic column and
 CC membrane, in order, and collecting fluid passing through the membrane.
 CC Angiostatin is useful for treating angiogenesis mediated diseases,
 CC including solid tumours, leukaemia, tumour metastases, benign tumours,
 CC rheumatoid arthritis, psoriasis, ocular angiogenic diseases, Osler-Webber

CC syndrome, myocardial angiogenesis, plaque neovascularisation,
 CC telangiectasia, haemophilic joints, angiodioma and wound granulation.
 CC As a centrifugation technique is not employed in the process, damage to
 CC the cells with concomitant release of undesirable biological materials
 CC such as cytochromes, pigments, enzymes, chemicals and other undesirable
 CC cellular constituents and debris, is prevented. Large scale recovery and
 CC purification of proteins is greater than that obtained from prior art
 CC methods. Active Angiostatin can be stored in buffers for extended periods
 CC of time, in vials or other containers, either in solution which may be
 CC liquid or frozen, or lyophilised
 XX
 SQ Sequence 260 AA;
 Query Match 100.0%; Score 1540; DB 4; Length 260;
 Best Local Similarity 100.0%; Pred. No. 1e-90;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGRGTGMSKTNGITCOKMSSTSPHRPRFPATHPSEGLSENYCRNPDN 60
 DB 1 VILSECKTGNGKNGRGTGMSKTNGITCOKMSSTSPHRPRFPATHPSEGLSENYCRNPDN 60
 QY 61 DPQPMCYTTDPKRYDYCDILCEBECCHMGSGENYDKISKTMSGLECOAMDOSPHAH 120
 DB 61 DPQPMCYTTDPKRYDYCDILCEBECCHMGSGENYDKISKTMSGLECOAMDOSPHAH 120
 QY 121 GYIPSKFPNNKLNKKNYCRNPDRELAPWCFTTDPNKRWELCDI PRCTTTPSSGPTYQCLK 180
 DB 121 GYIPSKFPNNKLNKKNYCRNPDRELAPWCFTTDPNKRWELCDI PRCTTTPSSGPTYQCLK 180
 QY 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGRAPWCHT 240
 DB 181 GTGENYRGNAVAVTSGHTCOHMSAQTPTHTERTPENFPCKNLDENYCRNPDGRAPWCHT 240
 QY 241 TNSQVMEYCKIIPSCDSSPV 260
 DB 241 TNSQVMEYCKIIPSCDSSPV 260

RESULT 3
 ADK40316
 ID ADK40316 standard; protein; 869 AA.
 AC ADK40316;
 XX
 AC ADK40316;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE C-terminal albumin-angiostatin fusion protein.
 XX
 KW cytosolic; vaccine; albumin fusion protein;
 KW angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer;
 KW collagen.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2003066085-A1.
 XX
 PD 14-AUG-2003.
 XX
 PF 07-FEB-2003; 2003MO-IB000433.
 XX
 PR 07-FEB-2002; 2002US-0355547P.
 XX
 PA (AVRT) AVENTIS BEHRING GMBH.
 PA (DELTA) DELTA BIOTECHNOLOGY LTD.
 XX
 PI Mertine P, Celik I, Kisker O, Sleep D, Hay J, Hauser H;
 XX
 DR WPI; 2003-731479/69.
 DR N-PSDB; ADK40315.
 XX
 PT New albumin fusion protein comprising an angiogenesis inhibiting peptide
 PT and an albumin having an albumin activity, or their fragments or

PT variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.
XX
PS Disclosure; Fig 8; 136pp; English.
XX
CC The invention relates to an albumin fusion protein comprising an
CC angiogenesis inhibiting peptide and an albumin having an albumin
CC activity, or their fragments or variants. The albumin fusion proteins,
CC compositions, vaccines and methods are useful for treating angiogenesis-
CC dependent tumor, e.g. cancer. This sequence represents an C-terminal
CC albumin-angiotensin fusion protein.
XX
SQ Sequence 869 AA;

Query Match 99.8%; Score 1537; DB 7; Length 869;
Best Local Similarity 99.6%; Pred. No. 4.9e-90;
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMSTKNGITCQWMSSTSPHRRFSPATHPSBGLBENYCRNPDN 60
DB 610 VYLSECKTGNGKNYRGTMSTKNGITCQWMSSTSPHRRFSPATHPSBGLBENYCRNPDN 669
QY 61 DPQGWCTTTPPEKRYDYCDILCEBECMHCSENYDGIKSTMSGLBQAMDSPRAH 120
DB 670 DPQGWCTTTPPEKRYDYCDILCEBECMHCSENYDGIKSTMSGLBQAMDSPRAH 729
QY 121 GYIPSKFPKNLKKNYCNPDRRLRPMCFCTTDPNKRWELCDIPRCTPPSSGPTYOCLK 180
DB 730 GYIPSKFPKNLKKNYCNPDRRLRPMCFCTTDPNKRWELCDIPRCTPPSSGPTYOCLK 789
QY 181 GTGENYRGNVAVTSGHTCQWMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
DB 790 GTGENYRGNVAVTSGHTCQWMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 849
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 850 TNSQVRWEYCKIPSCDSSPV 869

RESULT 4
ADK40314
ID ADK40314 standard; protein; 869 AA.
XX
AC ADK40314;
XX
DT 06-MAY-2004 (first entry)
XX
DE N-terminal angiotensin-albumin fusion protein.
XX
KW cyostatic; vaccine; albumin fusion protein;
KW angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer;
KW collagen.
XX
OS Homo sapiens.
OS Synthetic.
XX
PM WO2003066085-A1.
XX
PD 14-AUG-2003.
XX
PF 07-FEB-2003; 2003WO-1B000433.
XX
PR 07-FEB-2002; 2002US-0355547P.
XX
PA (AVENTIS) AVENTIS BEHRING GMBH.
XX (DELTA 2) DELTA BIOTECHNOLOGY LTD.
XX
PI Mertins P, Celik I, Kisker O, Sleep D, Hay J, Hauser H;
XX WPI; 2003-731479/69.
XX DR N-PSDB; ADK40313.
XX
PT New albumin fusion protein comprising an angiogenesis inhibiting peptide
PT and an albumin having an albumin activity, or their fragments or

PT variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.
XX
PS Disclosure; Fig 6; 136pp; English.
XX
CC The invention relates to an albumin fusion protein comprising an
CC angiogenesis inhibiting peptide and an albumin having an albumin
CC activity, or their fragments or variants. The albumin fusion proteins,
CC compositions, vaccines and methods are useful for treating angiogenesis-
CC dependent tumor, e.g. cancer. This sequence represents an N-terminal
CC angiotensin-albumin fusion protein.
XX
SQ Sequence 869 AA;

Query Match 99.8%; Score 1537; DB 7; Length 869;
Best Local Similarity 99.6%; Pred. No. 4.9e-90;
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNYRGTMSTKNGITCQWMSSTSPHRRFSPATHPSBGLBENYCRNPDN 60
DB 25 VYLSECKTGNGKNYRGTMSTKNGITCQWMSSTSPHRRFSPATHPSBGLBENYCRNPDN 84
QY 61 DPQGWCTTTPPEKRYDYCDILCEBECMHCSENYDGIKSTMSGLBQAMDSPRAH 120
DB 85 DPQGWCTTTPPEKRYDYCDILCEBECMHCSENYDGIKSTMSGLBQAMDSPRAH 144
QY 121 GYIPSKFPKNLKKNYCNPDRRLRPMCFCTTDPNKRWELCDIPRCTPPSSGPTYOCLK 180
DB 145 GYIPSKFPKNLKKNYCNPDRRLRPMCFCTTDPNKRWELCDIPRCTPPSSGPTYOCLK 204
QY 181 GTGENYRGNVAVTSGHTCQWMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
DB 205 GTGENYRGNVAVTSGHTCQWMSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 264
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 265 TNSQVRWEYCKIPSCDSSPV 284

RESULT 5
AAG79748
ID AAG79748 standard; protein; 260 AA.
XX
AC AAG79748;
XX
DT 18-MAR-2003 (first entry)
XX
DE Human plasma protein kring domain 1-3, K1-3.
XX
KW Human; plasminogen; angiotensin; neovascularization; kring domain;
KW cell proliferation; viral vector; replication-defective; cancer; tumour.
XX
OS Homo sapiens.
OS
XX
PN WO200288173-A2.
XX
PD 07-NOV-2002.
XX
PF 29-APR-2002; 2002WO-US013461.
XX
PR 30-APR-2001; 2001US-028673P.
XX 05-APR-2002; 2002US-0370634P.
XX
PA (CELL-) CELL GENESYS INC.
XX
PI Chang B, Wu W, Macarthur J, Patel S, Jooss K, Mendez M;
XX WPI; 2003-129131/12.
XX DR N-PSDB; ABA00776.
XX
PT New recombinant viral vector expressing human angiotensin useful for
PT inhibiting angiogenesis in a mammalian subject with cancer or tumor.
XX
PS Disclosure; Page 75-76; 83pp; English.

PF 30-SEP-1998; 98WO-US020464.
 XX
 PR 01-OCT-1997; 97US-0060609P.
 XX
 PA (SEARL) SEARLE & CO G D.
 XX
 PI Bolanowski MA, Caparon MH, Caspersen GF, Gregory SA, Klein BK,
 PI McKearn JP;
 DR WPI, 1999-255098/21.
 XX
 PT New multifunctional proteins useful for treating angiogenic-mediated
 PT diseases.
 XX
 PS Claim 5; Page 97-98; 121pp; English.
 XX
 CC The specification describes multifunctional proteins which comprise
 CC combinations of angiotensin, endostatin, interferon, thrombospondin,
 CC interferon-inducible protein and platelet factor 4, and have anti-
 CC angiogenic and/or anti-tumor activity. The multifunctional protein may
 CC exhibit useful properties such as having similar or greater biological
 CC activity when compared to a single factor or by having improved half-life
 CC or decreased adverse side effects, or a combination of these properties.
 CC The proteins can be used for treating an angiogenic-mediated disease,
 CC e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis.
 CC They can also be used for inhibiting the production of tumor cells
 CC (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric,
 CC colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma)
 CC in a patient and for inhibiting tumor growth. The present sequence
 CC represents a multifunctional protein of the invention
 XX
 SQ Sequence 285 AA;

Query Match 99.7%; Score 1535; DB 2; Length 285;
 Best Local Similarity 99.6%; Pred. No. 2.3e-90;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNKNGKMTSKTKNGITCOKWSSTSPHRPRFSPATPSBGLSENYCRNDN 60
 DB 20 VYLSECKTGNKNGKMTSKTKNGITCOKWSSTSPHRPRFSPATPSBGLSENYCRNDN 79
 QY 61 DPOGWCCTTDPBPKRYDYCDLLECEBECMHCSGENYDCKISKTMGSLCQAMDSQSPRAH 120
 DB 80 DPOGWCCTTDPBPKRYDYCDLLECEBECMHCSGENYDCKISKTMGSLCQAMDSQSPRAH 139
 QY 121 GIYSKFPNKULKKNYCNPDRBLRPMCFITDPNKRMLCDIPRCTTTPSSGPTYOCLK 180
 DB 140 GIYSKFPNKULKKNYCNPDRBLRPMCFITDPNKRMLCDIPRCTTTPSSGPTYOCLK 199
 QY 181 GTGENYRGNVAVTYSGHTCOHWSAQTPHTHRTENPFCKLIDENYCNPDGKAPWCHT 240
 DB 200 GTGENYRGNVAVTYSGHTCOHWSAQTPHTHRTENPFCKLIDENYCNPDGKAPWCHT 259
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 DB 260 TNSQVRWEYCKIPSCDSSPV 279

RESULT 8
 AAR83961
 ID AAR83961 standard; protein; 339 AA.
 XX
 AC AAR83961;
 XX
 DT 10-MAR-1996 (first entry)
 XX
 DE Human plasminogen peptide fragment.
 XX
 KW Angiostatin; plasminogen; endothelial inhibitor; therapeutic;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX

PN W09529242-A1.
 XX
 PD 02-NOV-1995.
 XX
 XX 26-APR-1995; 95WO-US005107.
 PF
 XX 26-APR-1994; 94US-00248629.
 PR 20-OCT-1994; 94US-00326785.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Orellilly MS, Folkman MW, Sim KL, Cao Y;
 PI WPI, 1995-382990/49.
 DR
 XX
 PT Endothelial inhibitor Angiostatin - useful to treat angiogenic mediated
 PT disease esp. angiogenesis and cancer.
 XX
 PS Claim 4; Page 81-82; 108pp; English.

CC The sequence represents a plasminogen fragment which is compared with the
 CC corresponding plasminogen fragments of monkey (AAR83962), pig (AAR83963)
 CC and cattle (AAR83964) origin (in Fig.2), as well as the with the first
 CC 339 amino acids of mouse angiotensin (AAR83960) (i.e. aa's 98-436 of the
 CC complete 812 aa plasminogen molecule AAR83959). Human angiotensin is a
 CC plasminogen fragment starting at aa 97 or 99 of the complete plasminogen
 CC molecule. Angiostatin is an endothelial inhibitor, which reversibly
 CC inhibits proliferation of endothelial cells and thereby inhibits
 CC angiogenesis. It is useful in the treatment of a human or animal with
 CC angiogenic mediated disease e.g. arthritis, macular degeneration,
 CC diabetic retinopathy or cancer. Cells comprising angiotensin-coding
 CC sequences are useful for gene therapy of primary tumors
 XX
 SQ Sequence 339 AA;

Query Match 99.7%; Score 1535; DB 2; Length 339;
 Best Local Similarity 99.6%; Pred. No. 2.7e-90;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNKNGKMTSKTKNGITCOKWSSTSPHRPRFSPATPSBGLSENYCRNDN 60
 DB 1 VYLSECKTGNKNGKMTSKTKNGITCOKWSSTSPHRPRFSPATPSBGLSENYCRNDN 60
 QY 61 DPOGWCCTTDPBPKRYDYCDLLECEBECMHCSGENYDCKISKTMGSLCQAMDSQSPRAH 120
 DB 61 DPOGWCCTTDPBPKRYDYCDLLECEBECMHCSGENYDCKISKTMGSLCQAMDSQSPRAH 120
 QY 121 GIYSKFPNKULKKNYCNPDRBLRPMCFITDPNKRMLCDIPRCTTTPSSGPTYOCLK 180
 DB 121 GIYSKFPNKULKKNYCNPDRBLRPMCFITDPNKRMLCDIPRCTTTPSSGPTYOCLK 180
 QY 181 GTGENYRGNVAVTYSGHTCOHWSAQTPHTHRTENPFCKLIDENYCNPDGKAPWCHT 240
 DB 181 GTGENYRGNVAVTYSGHTCOHWSAQTPHTHRTENPFCKLIDENYCNPDGKAPWCHT 240
 QY 241 TNSQVRWEYCKIPSCDSSPV 260
 DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 9
 AAM07581
 ID AAM07581 standard; protein; 339 AA.
 XX
 AC AAM07581;
 XX
 DT 24-JUN-1997 (first entry)
 XX
 DE N-Terminal angiotensin fragment.
 XX
 KW angiotensin; plasminogen; kringles; angiogenesis; cancer; arthritis;
 KW macular degeneration; diabetic retinopathy.
 XX


```

QY 61 DPGPWCYTTDPKRYDYCDILECEBECNHCSENGYDGIKSTKMSGLBEOAMDOSPFAH 120
DB 61 DPGPWCYTTDPKRYDYCDILECEBECNHCSENGYDGIKSTKMSGLBEOAMDOSPFAH 120
QY 121 GYIPSKFPNKNLKKNYCRNPDELRPWCTTDPNKRWEICDIPRCTTTPSSSGPTYQCCK 180
DB 121 GYIPSKFPNKNLKKNYCRNPDELRPWCTTDPNKRWEICDIPRCTTTPSSSGPTYQCCK 180
QY 181 GTGENYRGVAVTVSGHTCOHWSAQTPTHHTPENFPCKNDENYCRNPDGRAPWCHT 240
DB 181 GTGENYRGVAVTVSGHTCOHWSAQTPTHHTPENFPCKNDENYCRNPDGRAPWCHT 240
QY 241 TNSQVMEYCKIIPSCDSSPV 260
DB 241 TNSQVMEYCKIIPSCDSSPV 260

RESULT 11
AAM50518
ID AAM50518 standard; protein; 339 AA.
AC AAM50518;
DT 12-MAR-2002 (first entry)
DE Human angiotactin.
KW Angiotactin; plasminogen; human; angiogenesis; endothelial cell;
KW cell proliferation; inhibitor; tumour; antiproliferative; cytostatic;
KW vasotropic; antitumour; dermatological; antinflammatory; antidiabetic;
KW antithrombotic; antithrombotic; ophthalmological; vulnereary; antitumor;
KW antithrombotic; antithrombotic; gynaecological; antipruritic;
KW cardiant; contraceptive; therapy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Region 6..255
FT /label= Kring1e-1-3
FT 6..165
FT /label= Kring1e-1-2
FT 6..84
FT /label= Kring1e-1
FT 88..255
FT /label= Kring1e-2-3
FT 88..165
FT /label= Kring1e-2
FT 178..255
FT /label= Kring1e-3
XX
XX US2001029246-A1.
XX
XX 11-OCT-2001.
XX
XX 16-FEB-2001; 2001US-00788142.
XX
XX 30-MAY-1997; 97US-00866735.
XX 24-APR-1998; 98US-00066028.
XX 11-MAY-1999; 99US-00309821.
XX 22-JUN-1999; 99US-00338387.
XX
XX (OREI/) O'REILLY M S.
XX (FOLE/) FOLKMAN M J.
XX (CAO/) CAO Y.
XX
XX O'reilly MS, Folkman MJ, Cao Y;
XX
XX MPI; 2001-647990/74.
XX
XX Inhibiting endothelial cell proliferation, useful for treating angiogenic
XX mediated diseases such as cancer, arthritis, comprises administering
XX plasminogen fragment corresponding to kring1e structures of plasminogen
XX molecule.

```

```

XX
XX Example 27; Fig 2A-C; 70pp; English.
PS
XX The present sequence is that of human angiotactin. A claimed method of
CC inhibiting endothelial cell proliferation involves administering a
CC plasminogen fragment (PF) having an amino acid sequence similar to the
CC kring1e 1-5 region of a plasminogen molecule. This includes a protein,
CC termed angiotactin, defined by its ability to overcome the angiogenic
CC activity of endogenous growth factors and by its amino acid sequence
CC homology and structural similarity to an internal portion of plasminogen,
CC beginning at approximately amino acid 98. The PF is preferably derived
CC from mouse, human, Rhesus monkey, pig or cattle (see AAM50516-21). It is
CC used in methods and compositions for the treatment of an angiogenic-
CC mediated disease, including haemangioma, solid tumours, blood-borne
CC tumours, leukaemia, metastasis, telangiectasia, psoriasis,
CC atherosclerosis, scleroderma, pyogenic granuloma, myocardial
CC angiogenesis, Crohn's disease, plaque neovascularisation, coronary
CC collateral, cerebral collaterals, arteriovenous malformations, ischaemic
CC limb angiogenesis, corneal diseases, rubeosis, neovascular glaucoma,
CC diabetic retinopathy, corneal graft rejection, retrolental fibroplasia,
CC haemophilic joints, rheumatoid arthritis, diabetic neovascularisation,
CC Osler-Webber syndrome, macular degeneration, wound healing, peptic ulcer,
CC Helicobacter pylori related diseases, fractures, keloids, vasculogenesis,
CC fever. Angiotactin is also useful as a birth control agent by preventing
CC vascularisation required for embryo implantation. The compositions are
CC particularly useful for treating or repressing the growth of tumours.
CC Administration of angiotactin to a human or animal with prevascularised
CC metastasized tumours will prevent the growth or expansion of those
XX tumours. Gene therapy methods are also included in the invention
XX
XX Sequence 339 AA;
XX
XX Query Match 99.7%; Score 1535; DB 4; Length 339;
XX Best Local Similarity 99.6%; Pred. No. 2.7e-90;
XX Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 VYLSECKTGNGKNYGTMSKTNGITCQKWSSTSPRRPSPATPSBGLSENYCNPNN 60
DB 1 VYLSECKTGNGKNYGTMSKTNGITCQKWSSTSPRRPSPATPSBGLSENYCNPNN 60
QY 61 DPGPWCYTTDPKRYDYCDILECEBECNHCSENGYDGIKSTKMSGLBEOAMDOSPFAH 120
DB 61 DPGPWCYTTDPKRYDYCDILECEBECNHCSENGYDGIKSTKMSGLBEOAMDOSPFAH 120
QY 121 GYIPSKFPNKNLKKNYCRNPDELRPWCTTDPNKRWEICDIPRCTTTPSSSGPTYQCCK 180
DB 121 GYIPSKFPNKNLKKNYCRNPDELRPWCTTDPNKRWEICDIPRCTTTPSSSGPTYQCCK 180
QY 181 GTGENYRGVAVTVSGHTCOHWSAQTPTHHTPENFPCKNDENYCRNPDGRAPWCHT 240
DB 181 GTGENYRGVAVTVSGHTCOHWSAQTPTHHTPENFPCKNDENYCRNPDGRAPWCHT 240
QY 241 TNSQVMEYCKIIPSCDSSPV 260
DB 241 TNSQVMEYCKIIPSCDSSPV 260

RESULT 12
ADG47024
ID ADG47024 standard; protein; 339 AA.
AC ADG47024;
DT 11-MAR-2004 (first entry)
DE Human angiotactin protein.
XX
XX Angiotactin; cell proliferation; angiogenic-mediated disease; cancer;
XX arthritis; macular degeneration; diabetic retinopathy; psoriasis;
XX scleroderma; Crohn's disease; wounds; peptic ulcer; fracture;
XX gene therapy; plasminogen; cytostatic; ophthalmological; dermatological;
XX antinflammatory; vulnereary; human.

```

| | |
|---------------------------|---|
| XX | Homo sapiens. |
| OS | US2003064926-A1. |
| XX | |
| PN | 03-APR-2003. |
| XX | |
| PD | 22-APR-2002; 2002US-00127066. |
| XX | |
| PF | 26-APR-1994; 94US-00248629. |
| XX | |
| PR | 20-OCT-1994; 94US-00326785. |
| XX | |
| PR | 26-APR-1995; 95US-00429743. |
| XX | |
| PR | 08-MAR-1996; 96US-00612788. |
| XX | |
| PR | 30-MAY-1997; 97US-00866735. |
| XX | |
| PR | 24-APR-1998; 98US-00066028. |
| XX | |
| PR | 11-MAY-1999; 99US-00309821. |
| XX | |
| PR | 17-JUN-1999; 99US-00335325. |
| XX | |
| PR | 12-FEB-2001; 2001US-00383817. |
| XX | |
| PA | (FOLK/) FOLKMAN M J. |
| XX | |
| PA | (OREI/) O'REILLY M S. |
| XX | |
| PA | (CAOY/) CAO Y. |
| XX | |
| PA | (SIMK/) SIM K L. |
| XX | |
| PI | Folkman MJ, O'Reilly MS, Cao Y, Sim KL; |
| XX | |
| DR | WPI; 2003-540796/51. |
| XX | |
| PT | Inhibiting endothelial cell proliferation, useful for treating cancer, |
| XX | |
| PT | architect or diabetic retinopathy, comprises administering to an |
| XX | |
| PT | endothelial cell a proliferation-inhibiting amount of an angioetatin |
| XX | |
| PT | fragment. |
| XX | |
| PS | Example 27; SEQ ID NO 3; 96pp; English. |
| XX | |
| CC | The present invention relates to endothelial inhibitors called |
| XX | |
| CC | angiotatin which reversibly inhibit proliferation of endothelial cells. |
| XX | |
| CC | The invention is useful for diagnosing and treating angiogenic-mediated |
| XX | |
| CC | diseases such as cancer, arthritis, macular degeneration, diabetic |
| XX | |
| CC | retinopathy, psoriasis, scleroderma, Crohn's disease, wounds, peptic |
| XX | |
| CC | ulcer and fractures. The invention is also useful in gene therapy. The |
| XX | |
| CC | present sequence is the human angiotatin protein. |
| XX | |
| SQ | Sequence 339 AA; |
| Query Match | 99.7%; Score 1535; DB 7; Length 339; |
| Best Local Similarity | 99.6%; Pred. No. 2.7e-90; |
| Matches 259; Conservative | 0; Mismatches 1; Indels 0; Gaps 0; |
| QY | 1 VYLSECKTGNKGNYGWTMSKTNGKITTCOMSSSTPHRPFPSPATHPBSGLENNYCRNPDN 60 |
| DB | 1 VYLSCKTGNGNGNYGWTMSKTNGKITTCOMSSSTPHRPFPSPATHPBSGLENNYCRNPDN 60 |
| QY | 61 DPOGFWCYTTPDEKRYDYCDLIECEBECMHSGENYDGKISKTMSGLECOANDSOPHAA 120 |
| DB | 61 DPOGFWCYTTPDEKRYDYCDLIECEBECMHSGENYDGKISKTMSGLECOANDSOPHAA 120 |
| QY | 121 GTIPSKFPKNKKXNYCRRPDELRLPWCTTDPPNRKWLCDIPRCTTPPSSGPYYOCUK 180 |
| DB | 121 GTIPSKFPKNKKXNYCRRPDELRLPWCTTDPPNRKWLCDIPRCTTPPSSGPYYOCUK 180 |
| QY | 181 GYGENYRGVAVTVASGHTCOHNSAQTPTHERTPENFPCKNLIDENYCRRNPDKRAPWCHT 240 |
| DB | 181 GYGENYRGVAVTVASGHTCOHNSAQTPTHERTPENFPCKNLIDENYCRRNPDKRAPWCHT 240 |
| QY | 241 TNSOVRMEYCKIIPSCDSSFV 260 |
| DB | 241 TNSOVRMEYCKIIPSCDSSFV 260 |

ID ADM11543 standard; protein; 339 AA.
 AC ADM11543;
 XX 20-MAY-2004 (first entry)
 DT
 XX Human plasminogen fragment (angiotectin).
 DE
 XX endothelial cell proliferation; plasminogen; kringle 1-5;
 KW angiotectin-mediated disease; cancer; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; macular degeneration; corneal graft rejection;
 KW neovascular glaucoma; retrolental fibroplasia; rubeosis;
 KW Osler-Weber syndrome; myocardial angiogenesis; murine; human; Rhesus;
 KW porcine; bovine; angiotectin.
 XX
 OS Homo sapiens.
 XX
 PM US2004023877-A1.
 PD
 XX 05-FEB-2004.
 XX
 XX 27-MAR-2003; 2003US-00401108.
 PF
 XX 26-APR-1994; 94US-00248629.
 PR 20-OCT-1994; 94US-00326785.
 PR 26-APR-1995; 95US-00429743.
 PR 08-MAR-1996; 96US-00612788.
 PR 30-MAY-1997; 97US-00866735.
 PR 12-DEC-1997; 97US-00989477.
 PR 24-APR-1998; 98US-00060628.
 PR 11-MAY-1999; 99US-00309821.
 PR 22-JUN-1999; 99US-0038387.
 PR 16-FEB-2001; 2001US-00788142.
 XX
 XX (OREI/) O'REILLY M S.
 PA (POLK/) FOLKMAN M J.
 PA (CAOY/) CAO Y.
 XX
 XX O'Reilly MS, Folkman MJ, Cao Y;
 PI WPI; 2004-142673/14.
 DR
 XX
 PT New composition comprising an isolated nucleotide sequence that codes for
 PT a plasminogen fragment, useful for treating angiogenesis-dependent
 PT diseases including cancer, rheumatoid arthritis, psoriasis or macular
 PT degeneration.
 PS
 XX Example 18; SEQ ID NO 3; 78pp; English.
 XX
 XX The invention relates to a method of inhibiting endothelial cell
 CC proliferation, comprising administering to an endothelial cell a
 CC plasminogen fragment having an amino acid sequence similar to that of the
 CC kringle 1-5 region of plasminogen. The plasminogen fragment is derived
 CC from murine, human, Rhesus, porcine or bovine plasminogen. Also included
 CC are the following: (1) a method of treating a mammal with an angiogenic-
 CC mediated disease; (2) a therapeutic composition for inhibiting
 CC endothelial cell proliferation comprising a pharmaceutical excipient and
 CC the plasminogen fragment; and (3) a method of expressing a plasminogen
 CC fragment having an endothelial cell proliferation inhibiting activity.
 CC The method is useful for treating angiogenesis-dependent diseases
 CC including cancer. Angiogenesis-mediated diseases also include rheumatoid
 CC arthritis, psoriasis, diabetic retinopathy, macular degeneration, corneal
 CC graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis,
 CC Osler-Weber syndrome or myocardial angiogenesis. The present sequence
 CC represents human plasminogen fragment (angiotectin).
 XX
 SO Sequence 339 AA;
 Query Match 99.7%; Score 1535; DB 8; Length 339;
 Best local Similarity 99.6%; Pred. No. 2.7e-90;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0


```

Db      1 VYLSECKTNGKNYGTMSKTNGITTCQWMSSTSPHRRPSPATHPSEGLSENYCRNPDN 60
Qy      61 DQGWMCYTTPDEKRYDYCDILECEBECMHCSGENYDGIKSTMSGLEQAWDSOPHAN 120
Db      61 DQGWMCYTTPDEKRYDYCDILECEBECMHCSGENYDGIKSTMSGLEQAWDSOPHAN 120
Qy      121 GYIPSKFPNKNLKNKYCRNPDELRPWCFTTDPNKRWEICDIPRCTPPSPSGPTYQCILK 180
Db      121 GYIPSKFPNKNLKNKYCRNPDELRPWCFTTDPNKRWEICDIPRCTPPSPSGPTYQCILK 180
Qy      181 GTGENYRGNAVAVTSGHTCQWMSAQTPTHTERTPENPCKNIDENYCRNPDGKRAPWCHT 240
Db      181 GTGENYRGNAVAVTSGHTCQWMSAQTPTHTERTPENPCKNIDENYCRNPDGKRAPWCHT 240
Qy      241 TNSQVRWEYCKIPSCDSSPV 260
Db      241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 14
AA70255
ID      AAY70255 standard; protein; 363 AA.
XX
AC      AAY70255;
XX
DT      06-JUN-2000 (first entry)
XX
DE      Human angiotensin inhibitor, angiotensin.
XX
KW      Human; immunoglobulin gamma Fc fragment; angiotensin; immunofusion;
KW      angiotensin; inhibitor; cytostatic; antirheumatoid; antiarthritic;
KW      antipsoriatic; antidiabetic; ophthalmological; immunosuppressant;
KW      vasotropic; vulnerary; treatment; antiarteriosclerosis; tumour;
KW      metastasis; atherosclerosis; psoriasis; rheumatoid arthritis;
KW      ocular angiotensin disease; diabetic retinopathy; macular degeneration;
KW      myocardial angiotensin; plaque neovascularization; telangiectasia;
KW      wound granulation; keloid scar; gene therapy.
XX
XX      Homo sapiens.
OS
XX
PN      WO20011033-A2.
XX
PD      02-MAR-2000.
XX
PF      25-AUG-1999; 99WO-US019329.
XX
PR      25-AUG-1998; 98US-009783P.
XX
PA      (LEXI-) LEXINGEN PHARM CORP.
XX
PI      Lo K, Li Y, Gillies SD;
XX
PI      WPI: 2000-237616/20.
XX
DR      N-PSDB; AA551295.
XX
PT      Novel fusion protein of angiotensin or endostatin and an immunoglobulin
PT      Fc region, useful for treating conditions mediated by angiotensin, such
PT      as rheumatoid arthritis, tumors and macular degeneration.
XX
PS      Example 4; Page 45-46; 68pp; English.
XX
CC      The patent discloses a DNA molecule encoding a fusion protein comprising
CC      a signal sequence, an immunoglobulin Fc region, and an angiotensin
CC      inhibitor selected from angiotensin, endostatin, a plasminogen fragment
CC      having angiotensin activity, a collagen XVIII fragment having endostatin
CC      activity, or combinations of them. The fusion protein (immunofusion) is
CC      used to inhibit angiotensin and to treat diseases or conditions mediated
CC      by angiotensin. Conditions that may be treated include solid tumours,
CC      blood born tumours, tumour metastasis, benign tumours including
CC      haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic
CC      granulomas, rheumatoid arthritis, psoriasis, ocular angiotensin diseases
CC      e.g. diabetic retinopathy, retinopathy of prematurity, macular

```

```

CC      degeneration, corneal graft rejection, neovascular glaucoma, retrolental
CC      fibroplasia, rubecosis and Osher-Webber syndrome; myocardial angiotensin,
CC      plaque neovascularization, telangiectasia, haemophilic joints'
CC      angiofibroma, wound granulation, and excessive or abnormal stimulation of
CC      endothelial cells, intestinal cells, atherosclerosis, scleroderma and
CC      hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in
CC      gene therapy. The present sequence is a human angiotensin used in the
CC      construction of immunofusion containing human immunoglobulin gamma (1g)
CC      Fc fragment
XX
SQ      Sequence 363 AA;
XX
Query Match      99.7%; Score 1535; DB 3; Length 363;
Best Local Similarity 99.6%; Pred. No. 2.9e-90;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VYLSECKTNGKNYGTMSKTNGITTCQWMSSTSPHRRPSPATHPSEGLSENYCRNPDN 60
Db      2 VYLSECKTNGKNYGTMSKTNGITTCQWMSSTSPHRRPSPATHPSEGLSENYCRNPDN 61
Qy      61 DQGWMCYTTPDEKRYDYCDILECEBECMHCSGENYDGIKSTMSGLEQAWDSOPHAN 120
Db      62 DQGWMCYTTPDEKRYDYCDILECEBECMHCSGENYDGIKSTMSGLEQAWDSOPHAN 121
Qy      121 GYIPSKFPNKNLKNKYCRNPDELRPWCFTTDPNKRWEICDIPRCTPPSPSGPTYQCILK 180
Db      122 GYIPSKFPNKNLKNKYCRNPDELRPWCFTTDPNKRWEICDIPRCTPPSPSGPTYQCILK 181
Qy      181 GTGENYRGNAVAVTSGHTCQWMSAQTPTHTERTPENPCKNIDENYCRNPDGKRAPWCHT 240
Db      182 GTGENYRGNAVAVTSGHTCQWMSAQTPTHTERTPENPCKNIDENYCRNPDGKRAPWCHT 241
Qy      241 TNSQVRWEYCKIPSCDSSPV 260
Db      242 TNSQVRWEYCKIPSCDSSPV 261

RESULT 15
AA702106
ID      AAY02106 standard; protein; 364 AA.
XX
AC      AAY02106;
XX
DT      16-JUL-1999 (first entry)
XX
DE      A multifunctional protein of the invention.
XX
KW      Angiotensin; endostatin; interferon; thrombospondin;
KW      interferon-inducible protein; platelet factor 4; anti-angiotensin;
KW      anti-tumor; multifunctional protein; angiotensin-mediated disease; cancer;
KW      diabetic retinopathy; macular degeneration; arthritis;
KW      tumor cell production.
XX
XX      Synthetic.
OS
XX      Homo sapiens.
XX
PN      WO9916889-A1.
XX
PD      08-APR-1999.
XX
PF      30-SEP-1998; 98WO-US020464.
XX
PR      01-OCT-1997; 97US-0060609P.
XX
PA      (SEAR ) SEARLE & CO G D.
XX
PI      Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK;
PI      McKearn JP;
XX
XX      WPI: 1999-255098/21.
XX
DR      New multifunctional proteins useful for treating angiotensin-mediated
PT      diseases.

```

XX Claim 5; Page 101-102; 121pp; English.

CC The specification describes multifunctional proteins which comprise
CC combinations of angiotensin, endostatin, interferon, thrombospondin,
CC interferon-inducible protein and platelet factor 4, and have anti-
CC angiogenic and/or anti-tumor activity. The multifunctional protein may
CC exhibit useful properties such as having similar or greater biological
CC activity when compared to a single factor or by having improved half-life
CC or decreased adverse side effects, or a combination of these properties.
CC The proteins can be used for treating an angiogenic-mediated disease,
CC e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis.
CC They can also be used for inhibiting the production of tumor cells
CC (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric,
CC colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma)
CC in a patient and for inhibiting tumor growth. The present sequence
CC represents a multifunctional protein of the invention
XX

SQ Sequence 364 AA;

Query Match 99.7%; Score 1535; DB 2; Length 364;

Best Local Similarity 99.6%; Pred. No. 2.9e-90; Mismatches 1; Indels 0; Gaps 0;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGRGTMSTKNGITCQKMSSTSPHPRPSPATHPSEGLSENYCRNPDN 60
DB 3 VYLSECKTGNGKNGRGTMSTKNGITCQKMSSTSPHPRPSPATHPSEGLSENYCRNPDN 62
QY 61 DPQGPWCYTTDPKRYDYCDILFCEBECMHGSGENTDGI SKTMSGLBQAMDOSPHAH 120
DB 63 DPQGPWCYTTDPKRYDYCDILFCEBECMHGSGENTDGI SKTMSGLBQAMDOSPHAH 122
QY 121 GYIPSKFPMKNLKGQNCRNPDRELAPMCFTTDPNKRMELCDIPRCTPPSSGPTYQCLK 180
DB 123 GYIPSKFPMKNLKGQNCRNPDRELAPMCFTTDPNKRMELCDIPRCTPPSSGPTYQCLK 182
QY 181 GTGENYRGNAVAVTSGHTCQMSAQTPTHTERTPENPCNLDENYCRNPDGKRAPWCHT 240
DB 183 GTGENYRGNAVAVTSGHTCQMSAQTPTHTERTPENPCNLDENYCRNPDGKRAPWCHT 242
QY 241 TNSQVMEYCKIPSCDSSPV 260
DB 243 TNSQVMEYCKIPSCDSSPV 262

Search completed: January 25, 2006, 17:07:13
Job time : 138 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2006, 17:02:00 ; Search time 39 Seconds
(without alignments)
641.445 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSEKTXNGKNGRYRGTMSK.....TNSQVRWEYCKLRPSCDSSPV 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: plr1:*
2: plr2:*
3: plr3:*
4: plr4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 1535 | 99.7 | 810 | 1 | PLNU |
| 2 | 1442 | 93.6 | 810 | 2 | B30848 |
| 3 | 1292 | 83.9 | 790 | 1 | PLPG |
| 4 | 1291 | 82.8 | 812 | 1 | PLBO |
| 5 | 1274 | 82.7 | 812 | 1 | PLMS |
| 6 | 1237 | 80.3 | 810 | 2 | T18518 |
| 7 | 881 | 57.2 | 2869 | 2 | TI8518 |
| 8 | 797 | 51.8 | 728 | 1 | UH0579 |
| 9 | 782 | 50.4 | 728 | 1 | A35644 |
| 10 | 776.5 | 50.4 | 710 | 1 | IS1283 |
| 11 | 776 | 49.8 | 728 | 1 | A60185 |
| 12 | 766.5 | 49.8 | 716 | 1 | JCS061 |
| 13 | 754.5 | 49.0 | 411 | 2 | IS1285 |
| 14 | 753.5 | 48.9 | 716 | 1 | A40332 |
| 15 | 749 | 48.6 | 4548 | 1 | S00657 |
| 16 | 739 | 48.0 | 711 | 1 | A47136 |
| 17 | 739 | 48.0 | 1420 | 2 | A32869 |
| 18 | 505 | 32.8 | 455 | 2 | A61545 |
| 19 | 499 | 32.4 | 460 | 2 | B61545 |
| 20 | 391.5 | 22.4 | 336 | 2 | S33879 |
| 21 | 372 | 24.2 | 625 | 2 | TBBO |
| 22 | 362.5 | 23.5 | 169 | 2 | A40522 |
| 23 | 357.5 | 23.2 | 618 | 2 | A35827 |
| 24 | 351 | 22.8 | 622 | 1 | TBRU |
| 25 | 348 | 22.6 | 617 | 2 | SI0511 |
| 26 | 309.5 | 19.1 | 562 | 1 | UKHTU |
| 27 | 295.5 | 20.2 | 559 | 1 | A35029 |
| 28 | 281.5 | 18.3 | 559 | 1 | A29941 |
| 29 | 278 | 18.1 | 120 | 2 | B61545 |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 271 | 17.6 | 89 | 2 | A60140 | plasma (EC 3.4.21 |
| 31 | 268 | 17.4 | 123 | 2 | C61545 | plasma (EC 3.4.21 |
| 32 | 241.5 | 15.7 | 937 | 2 | A45082 | neurotrophic recep |
| 33 | 240 | 15.6 | 943 | 2 | B45082 | neurotrophic recep |
| 34 | 237.5 | 15.4 | 946 | 1 | A47299 | for-related recep |
| 35 | 233 | 15.1 | 603 | 2 | S28941 | coagulation factor |
| 36 | 214 | 13.9 | 558 | 2 | JCS878 | plasma hyaluronan- |
| 37 | 210 | 13.6 | 560 | 1 | JC4795 | plasma hyaluronan- |
| 38 | 201 | 13.1 | 291 | 2 | I38098 | t-plasminogen acti |
| 39 | 198 | 12.9 | 615 | 1 | KFHU12 | coagulation factor |
| 40 | 190.5 | 12.4 | 593 | 2 | S45281 | coagulation factor |
| 41 | 188.5 | 12.2 | 655 | 2 | A46688 | hepatocyte growth |
| 42 | 178.5 | 11.6 | 806 | 2 | T18840 | hypothetical prote |
| 43 | 165 | 10.7 | 433 | 1 | UN0560 | u-plasminogen acti |
| 44 | 153 | 9.9 | 442 | 1 | UKRG | u-plasminogen acti |
| 45 | 151 | 9.8 | 432 | 1 | S18932 | u-plasminogen acti |

ALIGNMENTS

RESULT 1

PLNU
Plasma (EC 3.4.21.7) precursor [validated] - human
N:Alternate names: plasminogen precursor [plasminogen]
N:Contains: angiotensin; microplasmin; plasminogen
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text change 09-Jul-2004
C:Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A0
R:Peterson, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A>Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibr
A:Reference number: A35229; MUID:90202879; PMID:2318848
A:Accession: A35229
A:Molecule type: DNA
A:Residues: 1-810 <PEP>
A:Cross-references: UNIPROT:P00747; UNIPROT:Q9UBQ9; UNIPROT:Q9UMI2; UNIPARC:UPI000016ABE
A:Experimental source: leukocyte, lung fibroblast
R:Malagareti, N.; Bruno, U.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; T
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A>Title: Definition of the transcription initiation site of human plasminogen gene in 1
A:Reference number: I52242; MUID:91097523; PMID:2268308
A:Accession: I52242
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <MAL1>
A:Cross-references: UNIPARC:UPI0000062A8; GB:M62890; NID:G190092; PIDN:AAA36454.1; PID
R:Forstgen, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A>Title: Molecular cloning and characterization of a full-length cDNA clone for human p
A:Reference number: A26646; MUID:87162490; PMID:3030813
A:Accession: A26646
A:Molecule type: mRNA
A:Residues: 1-471, 'D', 473-810 <FOR>
A:Cross-references: UNIPARC:UPI000000DB8; GB:X05199; NID:G35530; PIDN:CAA28831.1; PID
A:Experimental source: liver
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A>Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A:Reference number: I45961; MUID:85023311; PMID:6148961
A:Accession: I45961
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 292-471, 'D', 473-810 <MAL2>
A:Cross-references: UNIPARC:UPI000016ABD4; GB:X02922; NID:G190112; PIDN:AAA60124.1; PID
A:Accession: I84609
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 367-419 <MAL3>
A:Cross-references: UNIPARC:UPI0000071CTD; GB:X02921; NID:G190110; PIDN:AAA60123.1; PID
R:Brundis, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A>Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,

A:Reference number: S03735; MUID:81212097; PMID:7238497
A:Accession: S03735
A:Molecule type: protein
A:Residues: 20-71,'E','73-76 <BRU>
A:Cross-references: UNIPARC:UPI0000172B8C
R:Schtrup-Jensen, L.; Petersen, T.E.; Magnusson, S.
Submitted to the Atlas, July 1977
A:Reference number: A00929
A:Accession: A00929
A:Molecule type: protein
A:Residues: 20-71,'E','73-85, 87-106,'D','108-360,'E',362-810 <SOT>
A:Cross-references: UNIPARC:UPI0000172B8D
R:Wiman, B.
Eur. J. Biochem. 76, 129-137, 1977
A:Title: Primary structure of the B-chain of human plasmin.
A:Reference number: A04627; MUID:77225245; PMID:142009
A:Accession: A04627
A:Molecule type: protein
A:Residues: 581-810 <WT1>
A:Cross-references: UNIPARC:UPI00001450E9
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
A:Title: Structural relationship between "glutamic acid" and "lysine" forms of human plasminogen.
A:Reference number: A04625; MUID:75093329; PMID:122932
A:Accession: A04625
A:Molecule type: protein
A:Residues: 20-50,'Q','51-71,'E','73-85, 87-100 <WT2>
A:Cross-references: UNIPARC:UPI0000172B8E
R:Wiman, B.; Wallen, P.
Eur. J. Biochem. 59, 539-547, 1975
A:Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen that is released during activation.
A:Reference number: A04626; MUID:76043692; PMID:126863
A:Accession: A04626
A:Molecule type: protein
A:Residues: 483-507,'E',509-604 <WT3>
A:Cross-references: UNIPARC:UPI0000172B8F
R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
J. Biol. Chem. 248, 1631-1633, 1973
A:Title: The primary structure of human plasminogen. II. The histidine loop of human plasminogen.
A:Reference number: A92125; MUID:73149248; PMID:4694729
A:Contents: annotation; active site
J:Groeskopf, W.R.; Summaria, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A:Title: Studies on the active center of human plasmin. Partial amino acid sequence of a fragment from human plasminogen.
A:Reference number: A92048; MUID:69234739; PMID:4240117
A:Contents: annotation; active site
R:Trexler, M.; Vail, Z.; Pathy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A:Title: Structure of the omega-amino-carboxylic acid-binding sites of human plasminogen.
A:Reference number: A92382; MUID:82213905; PMID:6919539
A:Contents: annotation; omega-amino-carboxylic acid binding sites
R:Vail, Z.; Pathy, L.
J. Biol. Chem. 259, 13690-13694, 1984
A:Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential for fibrin binding.
A:Reference number: A92455; MUID:85054794; PMID:6094526
A:Contents: annotation; fibrin binding site; omega-amino-carboxylic acid binding site
J:Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.; Schaller, J.
J. Biol. Chem. 271, 29461-29467, 1996
A:Title: Kringle domains of human angiotensinogen. Characterization of the anti-proliferative activity of the anti-proliferative kringle domain.
A:Reference number: A58811; MUID:97067211; PMID:8910613
A:Accession: A58811
A:Contents: annotation
R:Liljeholm, H.R.; Uggul, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A:Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (N-terminus).
A:Reference number: A58812; MUID:9548733; PMID:9548733
A:Accession: A58812
A:Contents: annotation
R:Tulinsky, A.; Mulichak, A.M.
Submitted to the Brookhaven Protein Data Bank, July 1991
A:Reference number: A51341; PDB:1PK4
A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
Submitted to the Brookhaven Protein Data Bank, July 1991

A:Reference number: A51488; PDB:2PK4
R:Wu, T.P.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, August 1993
A:Reference number: A51911; PDB:1PKR
A:Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
R:Padmanabhan, K.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, April 1994
A:Reference number: A52408; PDB:1PMK
A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
R:Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A65244; PDB:1CEA
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R:Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A:Reference number: A65245; PDB:1CEB
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R:Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A:Title: Crystal and molecular structure of human plasminogen kringles 4 refined at 1.9 Å
A:Reference number: A58819; PMID:92031502; PMID:1657148
A:Contents: annotation
R:Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A:Title: The refined structure of the epsilon-amino-caproic acid complex of human plasminogen activator
A:Reference number: A58818; PMID:92031503; PMID:1657149
A:Contents: annotation
R:de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.
Biochemistry 31, 270-279, 1992
A:Title: Crystal structure of the kringles 2 domain of tissue plasminogen activator at 2.0 Å
A:Reference number: A39483; PMID:92118803; PMID:1310033
R:Stec, B.; Teetler, M.M.; Whitlow, M.; Yamano, A.
submitted to the Brookhaven Protein Data Bank, June 1995
A:Reference number: A65980; PDB:1KRN
A:Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65803; PDB:1HPJ
A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
A:Title: (1)H-NMR assignments and secondary structure of human plasminogen kringles 1.
A:Reference number: S43645; PMID:94237157; PMID:8181475
A:Contents: annotation; conformation by (1)H-NMR, residues 96-184
R:Rejzante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A:Title: Solution structure of the epsilon-amino-hexanoic acid complex of human plasminogen activator
A:Reference number: A58817; PMID:94237158; PMID:8181476
A:Contents: annotation; conformation by (1)H-NMR
C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many of C:Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKU4 a d PIR:FGHGB).

C:Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITRUA2) immediately after synthesis, resulting in two chains connected by two disulfide bonds. Without the inhibitor, C:Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial conditions. C:Comment: Streptolysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiotensin. C:Comment: Solid tumors.

C:Genetics:
A:Gene: GDB:PLG
A:Cross-references: GDB:119498; OMIM:173350
A:Map position: 6q26-6q27
A:Features: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529/1
C:Function:
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of the walls of the graafian follicle; also activates the urokinase-type plasminogen activator; fibrinolysis
C:Superfamily: plasmin; kringles homology; plasminogen-related protein precursor homology

C/Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd
 F.1-96/Domain: plasminogen-related protein precursor homology <PLPH>
 F.1-19/Domain: signal sequence #status predicted <SIG>
 F.20-810/Product: plasminogen #status experimental <PRO>
 F.20-96/Domain: activation peptide #status experimental <APt>
 F.79-86/Product: angiotensin #status experimental <AST>
 F.97-580,581-810/Product: plasmin #status experimental <MAT>
 F.97-580/Domain: plasmin chain A #status experimental <CHA>
 F.103-181/Domain: kringle homology <KR1>

Query Match 99.7%; Score 1535; DB 1; Length 810;
 Best Local Similarity 99.6%; Pred. No. 1.6e-104;
 Matches 259; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

1 VLSSECKTNGKNGKRGTKNGITCQKMSSTSPRRPSPATHPSEGLSENNYCNPN 60
 98 VLSSECKTNGKNGKRGTKNGITCQKMSSTSPRRPSPATHPSEGLSENNYCNPN 157
 61 DPOGFWCYTTDEPERKDYCDILECEBCHGSGENYDGIKSTMSGLGCOAMDOSPHAH 120
 158 DPOGFWCYTTDEPERKDYCDILECEBCHGSGENYDGIKSTMSGLGCOAMDOSPHAH 217
 121 GYIPSKFPKKNLKKNYCRNPDELRPMWCTTDPNKKMELCDIPRCTPPSSGPTVQCCK 180
 218 GYIPSKFPKKNLKKNYCRNPDELRPMWCTTDPNKKMELCDIPRCTPPSSGPTVQCCK 277
 181 GGENYRGVAATVSGHTQHSACQPTHHERPENPCKNIDENYCRNPDGRAPWCHT 240
 278 GGENYRGVAATVSGHTQHSACQPTHHERPENPCKNIDENYCRNPDGRAPWCHT 337
 241 TNSQVRWEYCKIPSCDSSPV 260
 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 2

B30848
 Plasmin (BC 3.4.21.7) precursor - rhesus macaque
 C/Species: Macaca mulatta (rhesus macaque)
 C/Date: 31-Mar-1989 #sequence__revision 31-Mar-1989 #text_change 09-Jul-2004
 C/Accession: B32869; B30848
 R/Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
 J. Biol. Chem. 264, 5957-5965, 1989
 A>Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
 A/Reference number: A32869; MUID:89174660; PMID:2525643
 A/Accession: B32869
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-810 <TM>
 A:Cross-references: UNIPROT:P12545; UNIPARC:UPI0000131COP; GB:J04697; NID:9342272; PIND:
 C/Superfamily: Plasmin; kringle homology; plasminogen-related protein precursor homology
 C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F.1-96/Domain: plasminogen-related protein precursor homology <PLPH>
 F.1-9/Domain: signal sequence #status predicted <SIG>
 F.103-181/Domain: kringle homology <KR1>
 F.185-262/Domain: kringle homology <KR2>
 F.275-352/Domain: kringle homology <KR3>
 F.377-454/Domain: kringle homology <KR4>
 F.481-560/Domain: kringle homology <KR5>
 F.581-803/Domain: trypsin homology <TRY>
 F.49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32
 bonds: #status predicted
 F.622,665,760/Active site: His, Asp, Ser #status predicted

Query Match 93.6%; Score 1442; DB 2; Length 810;
 Best Local Similarity 93.1%; Pred. No. 9.4e-98;
 Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

1 VLSSECKTNGKNGKRGTKNGITCQKMSSTSPRRPSPATHPSEGLSENNYCNPN 60
 98 VLSSECKTNGKNGKRGTKNGITCQKMSSTSPRRPSPATHPSEGLSENNYCNPN 157
 61 DPOGFWCYTTDEPERKDYCDILECEBCHGSGENYDGIKSTMSGLGCOAMDOSPHAH 120

158 DPOGFWCYTTDEPERKDYCDILECEBCHGSGENYDGIKSTMSGLGCOAMDOSPHAH 217
 121 GYIPSKFPKKNLKKNYCRNPDELRPMWCTTDPNKKMELCDIPRCTPPSSGPTVQCCK 180
 218 GYIPSKFPKKNLKKNYCRNPDELRPMWCTTDPNKKMELCDIPRCTPPSSGPTVQCCK 277
 181 GGENYRGVAATVSGHTQHSACQPTHHERPENPCKNIDENYCRNPDGRAPWCHT 240
 278 GGENYRGVAATVSGHTQHSACQPTHHERPENPCKNIDENYCRNPDGRAPWCHT 337
 241 TNSQVRWEYCKIPSCDSSPV 260
 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 3

PLPG
 plasmin (BC 3.4.21.7) precursor - pig (fragment)
 N/Alternate names: plasminogen
 N/Contains: miniplasminogen
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 07-Sep-1990 #sequence__revision 01-Nov-1996 #text_change 09-Jul-2004
 C/Accession: S03733; S03737; A25834
 R/Schaller, J.; Marti, T.; Roeselele, S.J.; Kaempfer, U.; Rickli, E.E.
 Fibrinolysis 1, 91-102, 1987
 A>Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the c
 A/Reference number: S03733
 A/Accession: S03733
 A/Molecule type: protein
 A/Residues: 1-560 <SCH>
 A:Cross-references: UNIPROT:P06867; UNIPARC:UPI0000172B90
 R/Brunisholz, R.A.; Letch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.,
 Eur. J. Biochem. 114, 465-470, 1981
 A>Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
 A/Reference number: S03735; MUID:81212097; PMID:7238497
 A/Accession: S03737
 A/Molecule type: protein
 A/Residues: 1-57 <BRU>
 A:Cross-references: UNIPARC:UPI0000172B91
 R/Marti, T.; Schaller, J.; Rickli, E.E.
 Eur. J. Biochem. 149, 279-285, 1985
 A>Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
 A/Reference number: A25834; MUID:85203907; PMID:3846533
 A/Accession: A25834
 A/Molecule type: protein
 A/Residues: 450-790 <MAR>
 A:Cross-references: UNIPARC:UPI0000172B92
 C/Function:
 A/Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 us the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A/pathway: fibrinolysis
 C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C/Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote
 F.1-790/Product: plasminogen #status predicted <PRO>
 F.1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
 F.78-560/Product: activation peptide #status predicted <APt>
 F.84-162/Domain: kringle homology <KR1>
 F.166-243/Domain: kringle homology <KR2>
 F.256-333/Domain: kringle homology <KR3>
 F.358-435/Domain: kringle homology <KR4>
 F.450-790/Product: miniplasminogen #status experimental <MTN>
 F.461-540/Domain: kringle homology <KR5>
 F.561-790/Product: plasmin chain B #status experimental <BGH>
 F.561-793/Domain: trypsin homology <TRY>
 F.30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305
 bonds: #status predicted
 F.602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 83.9%; Score 1292; DB 1; Length 790;
 Best Local Similarity 81.4%; Pred. No. 8e-87;
 Matches 210; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

eful in treating solid tumors.

C:Function:

A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of the walls of the graafian follicle; also activates the urokinase-type plasminogen activator

A:Pathway: fibrinolysis

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology

C:Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydrolysis

F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-812/Product: plasminogen #status predicted <PRO>

F:20-96/Domain: activation peptide #status predicted <APT>

F:79-466/Product: angiotensin #status predicted <AST>

F:97-581/Product: plasmin #status predicted <MAT>

F:97-581/Domain: chain A #status predicted <ACH>

F:103-181/Domain: kringle homology <KR1>

F:185-262/Domain: kringle homology <KR2>

F:273-352/Domain: kringle homology <KR3>

F:377-454/Domain: kringle homology <KR4>

F:481-560/Domain: kringle homology <KR5>

F:582-812/Domain: chain B #status predicted <BGH>

F:582-805/Domain: trypsin homology <TRY>

F:49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32

Bonds: #status predicted

F:78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted

F:136,308/Binding site: carboxylate (Asn) (covalent) #status predicted

F:466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted

F:581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental

F:624,667,762/Active site: His, Asp, Ser #status predicted

Query Match

Best Local Similarity 82.7%; Score 1274; DB 1; Length 812;

Matches 208; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

Db 1 VLSECKTGNGKNGYKMTKNGITGQKWSSTSPRRPSPATPSEGLSENYCNPND 60

98 VLSSECKTGNGKNGYKMTKNGITGQKWSSTSPRRPSPATPSEGLSENYCNPND 157

61 DQGPWCYTTDPKRYDYCDILECEBCHGCGENYDGIKSTMSGLSECOANDSOPH 120

158 DQGPWCYTTDPKRYDYCDILECEBCHGCGENYDGIKSTMSGLSECOANDSOPH 217

121 GYIPKFPKPKLKKYCRNPDRELPRWCCTTPDNKMEKCDIPRCTPPSPSGPTQCL 180

218 GYIPKFPKPKLKKYCRNPDRELPRWCCTTPDNKMEKCDIPRCTPPSPSGPTQCL 277

181 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENFPCKNLIDENYCRNPDGRAPWC 240

278 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENFPCKNLIDENYCRNPDGRAPWC 337

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

F:185-262/Domain: kringle homology <KR2>
F:273-352/Domain: kringle homology <KR3>
F:377-454/Domain: kringle homology <KR4>
F:481-561/Domain: kringle homology <KR5>
F:582-803/Domain: trypsin homology <TRY>

Query Match

Best Local Similarity 80.3%; Score 1237; DB 2; Length 810;

Matches 201; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

Db 1 VLSECKTGNGKNGYKMTKNGITGQKWSSTSPRRPSPATPSEGLSENYCNPND 60

98 VLSSECKTGNGKNGYKMTKNGITGQKWSSTSPRRPSPATPSEGLSENYCNPND 157

61 DQGPWCYTTDPKRYDYCDILECEBCHGCGENYDGIKSTMSGLSECOANDSOPH 120

158 DQGPWCYTTDPKRYDYCDILECEBCHGCGENYDGIKSTMSGLSECOANDSOPH 217

121 GYIPKFPKPKLKKYCRNPDRELPRWCCTTPDNKMEKCDIPRCTPPSPSGPTQCL 180

218 GYIPKFPKPKLKKYCRNPDRELPRWCCTTPDNKMEKCDIPRCTPPSPSGPTQCL 277

181 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENFPCKNLIDENYCRNPDGRAPWC 240

278 GTGENYRGNAVAVTSGHTCQHSAGTPHTERTPENFPCKNLIDENYCRNPDGRAPWC 337

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

338 TMSQVMEYCKIPSCDSS 355

Db 338 TMSQVMEYCKIPSCDSS 355

241 TMSQVMEYCKIPSCDSS 258

RESULT 8

hepatocyte growth factor precursor [validated] - human

UN0579

Alternate names: hepatopoietin A; scatter factor

C:Species: Homo sapiens (man)

C:Date: 17-Aug-1992 #sequence revision 17-Aug-1992 #text change 09-Jul-2004

C:Accession: JH0579; J00333; A41140; B36677; A33512; A39006; PH0114; A37796; S06

R:Seki, T.; Hagiyama, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.

Gene 102, 213-219, 1991

A:Title: Organization of the human hepatocyte growth factor-encoding gene.

A:Reference number: JH0579; MUID:91340155; PMID:1831432

A:Accession: JH0579

A:Molecule type: DNA

A:Residues: 1-728 <SE>

A:Cross-references: UNIPROT:P14210, UNIPARC:UPI000000D92B, DDBJ:D90318

A:Note: The authors translated the codon GAA for residue 662 as Gly

R:Seki, T.; Hagiyama, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.

submitted to JPID, March 1991

A:Description: Organization of the human hepatocyte growth factor-encoding gene.

A:Reference number: J00333

A:Accession: J00333

A:Molecule type: DNA

A:Residues: 1-481, 'RT', 484-728 <SE2>

A:Cross-references: UNIPARC:UPI0000172B97

R:Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H.

Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991

A:Title: Evidence for the identity of human scatter factor and human hepatocyte growth factor

A:Reference number: A41140; MUID:9134393; PMID:1831266

A:Accession: A41140

A:Molecule type: mRNA

A:Residues: 1-728 <MT>

A:Cross-references: UNIPARC:UPI000000D92B, GB:M72339, NID:9337935, PIDN:AA64239.1; PID:

R:Seki, T.; Ihara, I.; Sugimura, A.; Shimomishi, M.; Nishizawa, T.; Asami, O.; Hagiyama, M.

Biochem. Biophys. Res. Commun. 172, 321-327, 1990

A:Title: Isolation and expression of cDNA for different forms of hepatocyte growth factor

A:Reference number: A36677; MUID:91205062; PMID:2145836

A:Accession: B36677

A:Molecule type: mRNA

A:Residues: 1-728 <SE3>

A:Cross-references: UNIPARC:UPI000000D92B; GB:M60718; NID:9184031; PIDN:AA52648.1; PID:

A:Accession: A36677

A:Molecule type: mRNA

A:Residues: 1-161, 167-728 <SE4>

A:Cross-references: UNIPARC:UPI0000146316; EMBL:X16323

A:Experimental source: leukocyte

R:Miyaazawa, K.; Tashibouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya

Biochem. Biophys. Res. Commun. 163, 967-973, 1989

A:Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth factor

A:Reference number: A33512; MUID:89392017; PMID:2528952

A:Accession: A33512

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-728 <MT>

A:Cross-references: UNIPARC:UPI000000D92B; GB:M29145; NID:9184041; PIDN:AA52650.1; PID:

R:Rubin, U.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hix

Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991

A:Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocyte

A:Reference number: A39006; MUID:91110540; PMID:1824873

A:Accession: A39006

A:Molecule type: mRNA

A:Residues: 1-161, 167-728 <RUB>

A:Cross-references: UNIPARC:UPI0000146316; GB:M55379

A:Experimental source: embryonic lung

R:Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama,

Biochem. Biophys. Res. Commun. 175, 660-667, 1991

A:Title: Identification of the N-terminal residue of the heavy chain of both native and

A:Reference number: PH0114; MUID:91207365; PMID:1826837

A:Accession: PH0114

A:Molecule type: protein

A:Residues: 32-43/53-58 <YOS>

A:Cross-references: UNIPARC:UPI0000172B98; UNIPARC:UPI0000172B99

A:Experimental source: plasma

R:Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.

J. Cell Biol. 111, 2097-2108, 1990

A:Title: Scatter factor: molecular characteristics and effect on the invasiveness of epi

A:Reference number: A37796; MUID:91035621; PMID:2146276

A:Accession: A37796

A:Molecule type: protein

A:Residues: 86-91, 329-344, 356-363, 'XX', 366-370, 425-434, 442-447, 'X', 449-450, 543-546, 'X', 5

A:Cross-references: UNIPARC:UPI0000172B9A; UNIPARC:UPI0000172B9B; UNIPARC:UPI0000172B9C;

R:Nakamura, T.; Nishizawa, T.; Hagiyama, M.; Seki, T.; Shimomishi, M.; Sugimura, A.; Tash

Nature 342, 440-443, 1989

A:Title: Molecular cloning and expression of human hepatocyte growth factor.

A:Reference number: S06794; MUID:9006676; PMID:2531289

A:Accession: S06794

A:Molecule type: mRNA

A:Residues: 1-31, 'HK', 34-77, 'N', 79-292, 'V', 294-299, 'M', 301-316, 'A', 318-335, 'K', 337-386, 'A

A:Cross-references: UNIPARC:UPI000015624E; EMBL:X16323; NID:932081; PIDN:CAA34387.1; PID

A:Experimental source: liver

A:Note: The authors translated the codon CAG for residue 727 as Glu

R:Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birchm

Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992

A:Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact

A:Reference number: 159214; MUID:93087571; PMID:1280830

A:Accession: 159214

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-288, 'ET', 'HAR>

A:Cross-references: UNIPARC:UPI0000073BF9; GB:J02931; NID:9184033; PIDN:AA52649.1; PID:

R:Miyaazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.

Eur. J. Biochem. 197, 15-22, 1991

A:Title: An alternatively processed mRNA generated from human hepatocyte growth factor g

A:Reference number: S15443; MUID:91200041; PMID:1826553

A:Accession: S15443

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-288, 'ET' <MT2>

A:Cross-references: UNIPARC:UPI0000073BF9; EMBL:X57574; NID:932083; PIDN:CAA40802.1; PID

R:Shima, N.; Nagao, M.; Ogaki, F.; Tenda, E.; Murakami, A.; Higashio, K.

Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991

A:Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cloning

A:Reference number: 152253; MUID:92062058; PMID:1833383

A:Accession: 152253

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 161-166 <SHI>

A:Cross-references: UNIPARC:UPI00000353AB; GB:S62561; NID:9237996; PIDN:AA820169.1; PID:

C:Genetics:

A:Gene: GDB:RGF

A:Cross-references: GDB:127524; OMIM:142409

A:Map position: 7q21.1-7q21.1

A:Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1; 48

C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor

C:Function:

A:Description: stimulates mitosis of hepatocytes and other cells

A:Note: does not have proteinase activity

C:Keywords: hepatocyte growth factor/microphage stimulating protein 1; kringlike homolc

C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringlike; pyr

F:1-31/Domain: signal sequence #status predicted <SIG>

F:32-494/495-728/Product: hepatocyte growth factor #status experimental <MAT>

F:32-494/Domain: alpha chain #status experimental <ACH>

F:128-206/Domain: kringlike homology <KR1>

F:211-288/Domain: kringlike homology <KR2>

F:305-383/Domain: kringlike homology <KR3>

F:391-469/Domain: kringlike homology <KR4>

F:495-728/Domain: beta chain #status experimental <BCH>

F:395-716/Domain: tryptophan homology <TR>

F:32/modified site: pyrroline carboxylic acid (Gln) (in mature form) #status experimen

F:294, 402, 566, 653/binding site: carbohydrate (Asn) (covalent) #status predicted

F:487-604/Disulfide bonds: #status predicted

Query Match 51.8%; Score 797; DB 1; Length 728;

Best Local Similarity 51.0%; Pred. No. 9; 4e-51;

Matches 134, Conservative 42, Mismatches 81, Indels 6, Gap# 4;

QY 2 YLSBCKTNGKNYRGTMSKTNKGTTCQKWSSTSPRRPSPATPHSBGLSENYCRNPND 61
Db YLRNCTIGKGRSXYKGTAVITSKGIKCPWSSMIPHEHSFLPSSYRGKLDQENYCRNPGE 183
QY 62 PGPMPCYTTDDEKRVDCVDILIECEB-ECMHSGSENYDKISKTMSSGLECQAMDSQSPAH 120
Db EGGPMPCTFSPNEBRVEVDIPQCSBECEMTNGBSYRLMHTSSGKICQRMHDQTPHRH 243
QY 121 GYISKPEFNKULKNYCNPNPRELPMFCFTTDPNKRWECDIPRC--TTPPSSGP--TY 176
Db KFLPERYVDKFPDDNYCNPDPGQRRPMCYTIDPHTRMYCAIKTCADTMDTVPLETT 303
QY 177 QCLKGTGSENYRGNVAVTVSGHTCQHSNQTPTHTERTPEPNPCXNDENYCRNPDGKRA 236
Db ECIQGGGEGYGTAVTWTWNGIPQQRWDSQYFHEHDMTEFNKCKDLRENYCRNPDGSSSP 363
QY 237 WCHTTSQVRWEYC-KIPSCDS 258
Db 364 WCFITDPNIRVGYCSQIPNCDMS 386

RESULT 9
A35644
hepatocyte growth factor precursor - rat
N/Alternate names: hepatietin A; scatter factor
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004
C/Accession: A35644; S13211
R/Tanito, K.; Hagley, M.; Nishizawa, T.; Seki, T.; Shimomishi, M.; Shimizu, S.; Nakamura
Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A/Title: Deduced primary structure of rat hepatocyte growth factor and expression of the
A/Reference number: A35644; MUID:90222197; PMID:2139229
A/Accession: A35644
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-728 <TAS>
A/Cross-references: UNIPROT:P17945; UNIPARC:UPI000012C6D3; GB:D90102; GB:IM2987; NID:G222
R/Okajima, A.; Miyazawa, K.; Kitamura, N.
Eur. J. Biochem. 193, 375-381, 1990
A/Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA dur
A/Reference number: S13211; MUID:91031482; PMID:2146117
A/Accession: S13211
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-728 <OKA>
A/Cross-references: UNIPARC:UPI000012C6D3; EMBL:X54400; NID:G56353; PIDD:CAA38266.1; PIDD
C/Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C/Function:
A/Description: stimulates mitosis of hepatocytes and other cells
A/Note: does not have proteinase activity
C/Superfamily: hepatocyte growth factor/microphage stimulating protein 1; kringle homolo
C/Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyru
F:1-32/Domain: signal sequence #status predicted <SIG>
F:56-495/Product: hepatocyte growth factor #status predicted <MAT>
F:56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F:129-207/Domain: kringle homology <KR1>
F:212-289/Domain: kringle homology <KR2>
F:306-384/Domain: kringle homology <KR3>
F:392-470/Domain: kringle homology <KR4>
F:496-728/Domain: hepatocyte growth factor beta chain #status predicted <BGH>
F:496-719/Domain: tyrosin homology <TRY>
F:333/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status predi
F:293,403,559,556/Binding site: carbonylate (Asn) (covalent) #status predicted
F:488-607/Disulfide bonds: #status predicted

Query Match 50.8%; Score 782; DB 1; Length 728;
Best Local Similarity 49.8%; Pred. No. 1.2e-49;
Matches 132; Conservative 39; Mismatches 84; Indels 10; Gaps 4;

2 YLSBCKTNGKNYRGTMSKTNKGTTCQKWSSTSPRRPSPATPHSBGLSENYCRNPND 61

[illegible]

A:Molecule type: mRNA
A:Residues: 1-4548 <MCL>
A:Cross-references: UNIPROT:P08519, UNIPARC:UPI000013C499, GB:X06290, EMBL:X06696, NID:G
R.EACON, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A:Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to
A:Reference number: A28017, MUID:87204109, PMID:3472206
A:Accession: A28017
A:Molecule type: protein
A:Residues: 20-21, 'P', 23-34, 177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200, 292-314, 'W', 316-31
X, 4396-4401 <EAT>
A:Cross-references: UNIPARC:UPI0000172B0; UNIPARC:UPI0000172B1; UNIPARC:UPI0000172B2 #
R.Made, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, K.; Schwartz, K
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A:Title: 5' control regions of the apolipoprotein(a) gene and members of the related pla
A:Reference number: A47277, MUID:93165698, PMID:7679504
A:Accession: A47277
A:Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: UNIPARC:UPI0000062A8; GB:L07899; NID:g967973, PID:g967974
R.Margaret, N.; Acquati, F.; Magnagh, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Sacco
Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A:Title: Characterization by yeast artificial chromosome cloning of the linked apolipop
A:Reference number: A47233, MUID:93087573, PMID:1454851
A:Accession: I60906
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RE2>
A:Cross-references: UNIPARC:UPI0000062A8; GB:M90078; NID:g178786, PID:AAA35547.1, PID:
A:Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: A47233
A:Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RE5>
A:Cross-references: UNIPARC:UPI0000062A8; GB:M90079; NID:g178784, PID:AAA35546.1, PID:
R.Chinose, A.
Biochemistry 31, 3113-3118, 1992
A:Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated with
A:Reference number: I52415, MUID:92207924, PMID:1554698
A:Accession: I52415
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <R3>
A:Cross-references: UNIPARC:UPI0000062A8; GB:M86877; NID:g178780, PID:AA49909.1, PID:
A:Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: I65286
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <R4>
A:Cross-references: UNIPARC:UPI0000062A8; GB:M86878; NID:g178782, PID:AAA51749.1, PID:
C.Genetics:
A:Gene: GDB:LPA
A:Cross-references: GDB:120699; OMIM:152200
A:Map position: 6q26-6q27
A:Note: several genes closely linked on chromosome 6 are identical in the first coding e
rs of kringle repeats
C:Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C:Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-4548/Product: apolipoprotein(a) #status experimental <Mat>
F:148-105/Domain: kringle homology <KR1>
F:212-219/Domain: kringle homology <KR2>
F:256-333/Domain: kringle homology <KR3>
F:370-447/Domain: kringle homology <KR4>
F:484-561/Domain: kringle homology <KR5>
F:598-675/Domain: kringle homology <KR6>
F:712-789/Domain: kringle homology <KR7>
F:826-903/Domain: kringle homology <KR8>
F:940-1017/Domain: kringle homology <KR9>
F:1054-1131/Domain: kringle homology <KR10>
F:1168-1245/Domain: kringle homology <KR11>
F:1282-1359/Domain: kringle homology <KR12>

| | | | |
|----------------------|---------|----------|--------|
| F.11396-1473/Domain: | kringle | homology | <KR3> |
| F.1510-1587/Domain: | kringle | homology | <KR4> |
| F.1624-1701/Domain: | kringle | homology | <KR5> |
| F.1738-1815/Domain: | kringle | homology | <KR6> |
| F.1852-1929/Domain: | kringle | homology | <KR17> |
| F.1966-2043/Domain: | kringle | homology | <KR18> |
| F.2080-2157/Domain: | kringle | homology | <KR19> |
| F.2194-2271/Domain: | kringle | homology | <KR20> |
| F.2308-2385/Domain: | kringle | homology | <KR21> |
| F.2422-2499/Domain: | kringle | homology | <KR22> |
| F.2536-2613/Domain: | kringle | homology | <KR23> |
| F.2650-2727/Domain: | kringle | homology | <KR24> |
| F.2764-2841/Domain: | kringle | homology | <KR25> |
| F.2878-2955/Domain: | kringle | homology | <KR26> |
| F.2992-3069/Domain: | kringle | homology | <KR27> |
| F.3106-3183/Domain: | kringle | homology | <KR28> |
| F.3220-3297/Domain: | kringle | homology | <KR29> |
| F.3334-3411/Domain: | kringle | homology | <KR30> |
| F.3448-3525/Domain: | kringle | homology | <KR31> |
| F.3562-3639/Domain: | kringle | homology | <KR32> |
| F.3676-3753/Domain: | kringle | homology | <KR33> |
| F.3782-3859/Domain: | kringle | homology | <KR34> |
| F.3896-3973/Domain: | kringle | homology | <KR35> |
| F.4010-4087/Domain: | kringle | homology | <KR36> |
| F.4124-4201/Domain: | kringle | homology | <KR37> |
| F.4228-4307/Domain: | kringle | homology | <KR38> |
| F.4328-4541/Domain: | trypsin | homology | <TRY> |

Query Match 48.6%; Score 749; DB 1; Length 4548;

Best Local Similarity 41.2%; Pred. No. 1.8e-46;
Matches 129; Conservative 45; Mismatches 81; Indels 58; Gaps 5.

Matches 129; Conservative 45; Mismatches 81; Indels 58; Gaps 57

3 LSECKTGKNGVGTMSKNGITCQKMSSTSPHRRPSPATHPSEGLEENYCRNPNDP 62

3779 VQDCYHGQGSYRGSESTVTGTCQSSMSKTPHMHQRTLEYYPNGGLTRNYCRNDAEI 3838

63 QGPWCYTTDPKRYDYCDILECE-----BECM 89

3839 R-PWCYTMDPSVRWEYCNLTQCPMESTLLTPTVPVPSTELPSEEAFTENSTGVQDCY 389

90 HCSGENYDGI SKTMSGLECOAMDQS PHAGYIPSKFPNKU LKNYCNPNDRRLPWC F 149

3898 RGDGQSYRGTLLSTLTIGRTQSWSSMTPHWHRIPLYYPAGLTRNYCNPDAEIRPCWY 395

150 TTDPNKRWELCDIPRC-----TTP-----PRSSGPTYQ-CLKGTGEN 185

3958 TMDPSVRMEYCNLTRCPCVTSSVLTPTVAPVPSTEARSEGAAPPEKSPVIVQDCYHGGRS 4011

186 YRGNVAVTYSGHTCQHNSAQTPHTHERTPENFQCKNLDENYCRNPDGKAPMCHTINSQV 245

4018 YRGISSTVTGRTQSWSMIPHHQRTPEPNAGLITENYCRNPDGKQPMCYTTDPV 4077

246 RWEYCKI PSCDSS 258

```

4078 RMEYCNLTQCSST 4090

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

```

search completed: January 25, 2006, 11:10:57
job time : 40 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2006, 17:11:02 ; Search time 32 Seconds
(without alignments)
87.986 Million cell updates/sec

Title: US-09-502-176-2
Perfect score: 1540
Sequence: 1 VLSCKTGNKNGKNGYGTMSK.....TNSQVRWEYCKIPSCDSSPV 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10823074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------------|-------------------|
| 1 | 1535 | 99.7 | 339 | US-11-010-874-3 | Sequence 3, App1 |
| 2 | 1535 | 99.7 | 567 | US-10-995-561-764 | Sequence 764, App |
| 3 | 1535 | 99.7 | 791 | US-11-056-621-4 | Sequence 4, App1 |
| 4 | 1535 | 99.7 | 810 | US-10-995-561-761 | Sequence 761, App |
| 5 | 1535 | 99.7 | 810 | US-10-995-561-761 | Sequence 761, App |
| 6 | 1442 | 93.6 | 339 | US-11-010-874-4 | Sequence 4, App1 |
| 7 | 1296 | 84.2 | 339 | US-11-010-874-6 | Sequence 6, App1 |
| 8 | 1292 | 84.2 | 339 | US-11-010-874-5 | Sequence 5, App1 |
| 9 | 1274 | 82.7 | 339 | US-11-010-874-2 | Sequence 2, App1 |
| 10 | 1274 | 82.7 | 812 | US-11-010-874-1 | Sequence 1, App1 |
| 11 | 1001 | 65.0 | 168 | US-11-010-874-8 | Sequence 8, App1 |
| 12 | 954 | 61.8 | 168 | US-11-010-874-9 | Sequence 9, App1 |
| 13 | 952 | 61.8 | 168 | US-11-010-874-13 | Sequence 13, App1 |
| 14 | 896 | 58.2 | 168 | US-11-010-874-14 | Sequence 14, App1 |
| 15 | 883 | 57.3 | 168 | US-11-010-874-10 | Sequence 10, App1 |
| 16 | 881 | 57.2 | 168 | US-11-010-874-11 | Sequence 11, App1 |
| 17 | 847 | 55.0 | 168 | US-11-010-874-7 | Sequence 7, App1 |
| 18 | 801 | 52.0 | 160 | US-11-010-874-16 | Sequence 16, App1 |
| 19 | 799 | 51.9 | 160 | US-11-010-874-15 | Sequence 15, App1 |
| 20 | 797 | 51.8 | 160 | US-11-010-874-12 | Sequence 12, App1 |
| 21 | 797 | 51.8 | 728 | US-11-124-635-6 | Sequence 6, App1 |
| 22 | 797 | 51.8 | 728 | US-11-124-635-8 | Sequence 8, App1 |
| 23 | 797 | 51.8 | 728 | US-11-043-788-164 | Sequence 164, App |
| 24 | 749 | 48.6 | 1169 | US-10-995-561-609 | Sequence 609, App |
| 25 | 749 | 48.6 | 1169 | US-11-124-368A-228 | Sequence 228, App |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 26 | 711 | 46.2 | 308 | 7 | US-11-162-817-11 | Sequence 11, App1 |
| 27 | 643 | 41.8 | 648 | 7 | US-11-127-877-72 | Sequence 72, App1 |
| 28 | 531.5 | 34.5 | 290 | 7 | US-11-043-788-165 | Sequence 165, App |
| 29 | 524.5 | 34.1 | 296 | 7 | US-11-043-788-168 | Sequence 168, App |
| 30 | 320 | 20.8 | 516 | 6 | US-10-995-561-559 | Sequence 559, App |
| 31 | 309.5 | 20.1 | 527 | 6 | US-10-705-633-1 | Sequence 1, App1 |
| 32 | 309.5 | 20.1 | 527 | 6 | US-10-705-633-2 | Sequence 2, App1 |
| 33 | 309.5 | 20.1 | 527 | 6 | US-10-705-633-3 | Sequence 3, App1 |
| 34 | 309.5 | 20.1 | 562 | 6 | US-10-995-561-561 | Sequence 561, App |
| 35 | 293 | 19.0 | 482 | 6 | US-10-995-561-560 | Sequence 560, App |
| 36 | 270.5 | 17.6 | 79 | 7 | US-11-010-874-17 | Sequence 17, App1 |
| 37 | 258.5 | 16.8 | 86 | 7 | US-11-162-817-2 | Sequence 166, App |
| 38 | 246.5 | 16.0 | 205 | 7 | US-11-043-788-166 | Sequence 166, App |
| 39 | 219 | 14.2 | 61 | 6 | US-10-995-561-762 | Sequence 762, App |
| 40 | 219 | 14.2 | 136 | 6 | US-10-995-561-760 | Sequence 760, App |
| 41 | 205 | 13.3 | 293 | 6 | US-10-995-561-562 | Sequence 562, App |
| 42 | 204 | 13.2 | 291 | 6 | US-10-995-561-558 | Sequence 558, App |
| 43 | 198 | 12.9 | 641 | 7 | US-11-094-519A-29 | Sequence 29, App1 |
| 44 | 168 | 10.9 | 473 | 6 | US-10-509-464-5 | Sequence 5, App1 |
| 45 | 164.5 | 10.7 | 473 | 6 | US-10-509-464-6 | Sequence 6, App1 |

ALIGNMENTS

```

RESULT 1
US-11-010-874-3
; Sequence 3, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xiang
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; FILE REFERENCE: 5820.656
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963,115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510,620
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/528,647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-010-874-3
Query Match          99.7%; Score 1535, DB 7, Length 339;
Best Local Similarity 99.6%; Pred. No. 6.2e-119;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 VLSCKTGNKNGKNGYGTMSKNGITCKWSTSPHPPSPATPSBGLBENYCRNPN 60
1 VLSCKTGNKNGKNGYGTMSKNGITCKWSTSPHPPSPATPSBGLBENYCRNPN 60
61 DPGWCCTTPEKRYDCDILECEBCHGNGENYDKISKTMGLBQAMDSPHAF 120
61 DPGWCCTTPEKRYDCDILECEBCHGNGENYDKISKTMGLBQAMDSPHAF 120
121 GYIPKFPKNIKKNYCRNPDELRPWCTTDPNTRWEICDIPRCTTPSSGPTYOCL 180
121 GYIPKFPKNIKKNYCRNPDELRPWCTTDPNTRWEICDIPRCTTPSSGPTYOCL 180
181 GTGSEYRGNVAVTSGHCOHWSAOTPHTRSPENPCXNDENYCRNPDGKRAPWCHT 240
181 GTGSEYRGNVAVTSGHCOHWSAOTPHTRSPENPCXNDENYCRNPDGKRAPWCHT 240
241 TNSQVRWEYCKIPSCDSSPV 260
241 TNSQVRWEYCKIPSCDSSPV 260

```

```
RESULT 2
US-10-995-561-764
; Sequence 764, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 764
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-764

Query Match          99.7%; Score 1535; DB 6; Length 567;
Best Local Similarity 99.6%; Pred. No. 1e-118;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  VYLSCKTGNGKNYRGTMSTKNGITTCQKMSSTSPHPRFSPATPSBGLSENYCRNPDN 60
DB      98  VYLSCKTGNGKNYRGTMSTKNGITTCQKMSSTSPHPRFSPATPSBGLSENYCRNPDN 157
QY      61  DPQPMCTTDPDEKRYDCDILCEBECMHGSGENYDGKISKTMSGLECOANDSOPHAA 120
DB      158  DPQPMCTTDPDEKRYDCDILCEBECMHGSGENYDGKISKTMSGLECOANDSOPHAA 217
QY      121  GYIPSKFPKNLKKNYCRNPDLRPMCFCTTDPNKRMLCDIPRCTPPSSGPTYQCLK 180
DB      218  GYIPSKFPKNLKKNYCRNPDLRPMCFCTTDPNKRMLCDIPRCTPPSSGPTYQCLK 277
QY      181  GTGENYRGNAVAVTSGHTCOHMSAQTPTHRTPEPCKNLDENYCRNPDGKRAPWCHT 240
DB      278  GTGENYRGNAVAVTSGHTCOHMSAQTPTHRTPEPCKNLDENYCRNPDGKRAPWCHT 337
QY      241  TNSQVRMEYCKIIPSCDSSPV 260
DB      338  TNSQVRMEYCKIIPSCDSSPV 357

RESULT 3
US-11-056-621-4
; Sequence 4, Application US/11056621
; Publication No. US20050262592A1
; GENERAL INFORMATION:
; APPLICANT: Spencer, David
; APPLICANT: Dickey, Lynn F.
; APPLICANT: Gadsaka, John R.
; APPLICANT: Wang, Xiaowei
; APPLICANT: Cox, Kevin M.
; APPLICANT: Peele, Charles G.
; TITLE OF INVENTION: EXPRESSION OF PLASMINOGEN AND
; TITLE OF INVENTION: MICROPLASMINOGEN IN DUCKWEED
; FILE REFERENCE: 40989/274646
; CURRENT APPLICATION NUMBER: US/11/056,621
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,487
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of mature human plasminogen
```

```
US-11-056-621-4

Query Match          99.7%; Score 1535; DB 7; Length 791;
Best Local Similarity 99.6%; Pred. No. 1.4e-118;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  VYLSCKTGNGKNYRGTMSTKNGITTCQKMSSTSPHPRFSPATPSBGLSENYCRNPDN 60
DB      79  VYLSCKTGNGKNYRGTMSTKNGITTCQKMSSTSPHPRFSPATPSBGLSENYCRNPDN 138
QY      61  DPQPMCTTDPDEKRYDCDILCEBECMHGSGENYDGKISKTMSGLECOANDSOPHAA 120
DB      139  DPQPMCTTDPDEKRYDCDILCEBECMHGSGENYDGKISKTMSGLECOANDSOPHAA 198
QY      121  GYIPSKFPKNLKKNYCRNPDLRPMCFCTTDPNKRMLCDIPRCTPPSSGPTYQCLK 180
DB      199  GYIPSKFPKNLKKNYCRNPDLRPMCFCTTDPNKRMLCDIPRCTPPSSGPTYQCLK 258
QY      181  GTGENYRGNAVAVTSGHTCOHMSAQTPTHRTPEPCKNLDENYCRNPDGKRAPWCHT 240
DB      259  GTGENYRGNAVAVTSGHTCOHMSAQTPTHRTPEPCKNLDENYCRNPDGKRAPWCHT 318
QY      241  TNSQVRMEYCKIIPSCDSSPV 260
DB      319  TNSQVRMEYCKIIPSCDSSPV 338

RESULT 4
US-10-995-561-761
; Sequence 761, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 761
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-761

Query Match          99.7%; Score 1535; DB 6; Length 810;
Best Local Similarity 99.6%; Pred. No. 1.4e-118;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  VYLSCKTGNGKNYRGTMSTKNGITTCQKMSSTSPHPRFSPATPSBGLSENYCRNPDN 60
DB      98  VYLSCKTGNGKNYRGTMSTKNGITTCQKMSSTSPHPRFSPATPSBGLSENYCRNPDN 157
QY      61  DPQPMCTTDPDEKRYDCDILCEBECMHGSGENYDGKISKTMSGLECOANDSOPHAA 120
DB      158  DPQPMCTTDPDEKRYDCDILCEBECMHGSGENYDGKISKTMSGLECOANDSOPHAA 217
QY      121  GYIPSKFPKNLKKNYCRNPDLRPMCFCTTDPNKRMLCDIPRCTPPSSGPTYQCLK 180
DB      218  GYIPSKFPKNLKKNYCRNPDLRPMCFCTTDPNKRMLCDIPRCTPPSSGPTYQCLK 277
QY      181  GTGENYRGNAVAVTSGHTCOHMSAQTPTHRTPEPCKNLDENYCRNPDGKRAPWCHT 240
DB      278  GTGENYRGNAVAVTSGHTCOHMSAQTPTHRTPEPCKNLDENYCRNPDGKRAPWCHT 337
QY      241  TNSQVRMEYCKIIPSCDSSPV 260
DB      338  TNSQVRMEYCKIIPSCDSSPV 357

RESULT 5
```

| | | | | |
|-----------------------|--------------|--------------------|---------------|------------------|
| Query Match | 93.6% | Score 1442; | DB 7; | Length 339; |
| Best Local Similarity | 93.1% | Pred. No. 2.5e-11; | | |
| Matches 242; | Conservative | 9; | Mismatches 9; | Indels 0; Gaps 0 |

RESULT 8

Db 338 TDSQLRWEYCEIPSCSS 355

RESULT 11
US-11-010-874-8

/ Sequence 8, Application US/11010874
/ Publication No. US20050250694A1
/ GENERAL INFORMATION:
/ APPLICANT: Ma, Jian-Xing
/ TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
/ FILE REFERENCE: 5820.656
/ CURRENT APPLICATION NUMBER: US/11/010,874
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: 10/963,115
/ PRIOR FILING DATE: 2004-10-12
/ PRIOR APPLICATION NUMBER: 60/510,620
/ PRIOR FILING DATE: 2003-10-10
/ PRIOR APPLICATION NUMBER: 60/528,647
/ PRIOR FILING DATE: 2003-12-11
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 8
/ LENGTH: 168
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-010-874-8

Query Match 65.0%; Score 1001; DB 7; Length 168;
Best Local Similarity 99.4%; Pred. No. 1.5e-75;
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 86 CMHSGENVYDGKISTMTSGLECOAMDSPHAGYIPSKFPKNLKNYCRNPDRELRPW 147
Db 1 CMHSGENVYDGKISTMTSGLECOAMDSPHAGYIPSKFPKNLKNYCRNPDRELRPW 60

Qy 148 CETTDPNKRWELCDIPRCTTTPSSGPTYOCLKGTGENYRGNAVAVTSGHTCOHMSAOTP 207
Db 61 CETTDPNKRWELCDIPRCTTTPSSGPTYOCLKGTGENYRGNAVAVTSGHTCOHMSAOTP 120

Qy 208 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVRWEYCKIPSC 255
Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVRWEYCKIPSC 168

RESULT 12
US-11-010-874-9

/ Sequence 9, Application US/11010874
/ Publication No. US20050250694A1
/ GENERAL INFORMATION:
/ APPLICANT: Ma, Jian-Xing
/ TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
/ FILE REFERENCE: 5820.656
/ CURRENT APPLICATION NUMBER: US/11/010,874
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: 10/963,115
/ PRIOR FILING DATE: 2004-10-12
/ PRIOR APPLICATION NUMBER: 60/510,620
/ PRIOR FILING DATE: 2003-10-10
/ PRIOR APPLICATION NUMBER: 60/528,647
/ PRIOR FILING DATE: 2003-12-11
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 9
/ LENGTH: 168
/ TYPE: PRT
/ ORGANISM: Rhesus monkey
US-11-010-874-9

Query Match 61.9%; Score 954; DB 7; Length 168;
Best Local Similarity 94.6%; Pred. No. 1.1e-71;
Matches 159; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 88 CMHSGENVYDGKISTMTSGLECOAMDSPHAGYIPSKFPKNLKNYCRNPDRELRPW 147
Db 1 CMHSGENVYDGKISTMTSGLECOAMDSPHAGYIPSKFPKNLKNYCRNPDRELRPW 60

Qy 148 CETTDPNKRWELCDIPRCTTTPSSGPTYOCLKGTGENYRGNAVAVTSGHTCOHMSAOTP 207
Db 61 CETTDPNKRWELCDIPRCTTTPSSGPTYOCLKGTGENYRGNAVAVTSGHTCOHMSAOTP 120

Qy 208 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVRWEYCKIPSC 255
Db 121 HTHETTPENFPCKNLIDENYCRNPDGRAPWCHTTNSQVRWEYCKIPSC 168

RESULT 13
US-11-010-874-13

/ Sequence 13, Application US/11010874
/ Publication No. US20050250694A1
/ GENERAL INFORMATION:
/ APPLICANT: Ma, Jian-Xing
/ TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
/ FILE REFERENCE: 5820.656
/ CURRENT APPLICATION NUMBER: US/11/010,874
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: 10/963,115
/ PRIOR FILING DATE: 2004-10-12
/ PRIOR APPLICATION NUMBER: 60/510,620
/ PRIOR FILING DATE: 2003-10-10
/ PRIOR APPLICATION NUMBER: 60/528,647
/ PRIOR FILING DATE: 2003-12-11
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 13
/ LENGTH: 160
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-010-874-13

Query Match 61.8%; Score 952; DB 7; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.5e-71;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CKTGKKNYRGMTSKTGITCOQKSSSPRRPSPATHSBEGLENYCRNPDPOGP 65
Db 1 CKTGKKNYRGMTSKTGITCOQKSSSPRRPSPATHSBEGLENYCRNPDPOGP 60

Qy 66 WCYTDPKRYDYCDILECEBECMHSGENVYDGKISTMTSGLECOAMDSPHAGYIPPS 125
Db 61 WCYTDPKRYDYCDILECEBECMHSGENVYDGKISTMTSGLECOAMDSPHAGYIPPS 120

Qy 126 KFPNKLKNYCRNPDRELRPWCFTTDPNKRWELCDIPRC 165
Db 121 KFPNKLKNYCRNPDRELRPWCFTTDPNKRWELCDIPRC 160

RESULT 14
US-11-010-874-14

/ Sequence 14, Application US/11010874
/ Publication No. US20050250694A1
/ GENERAL INFORMATION:
/ APPLICANT: Ma, Jian-Xing
/ TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
/ FILE REFERENCE: 5820.656
/ CURRENT APPLICATION NUMBER: US/11/010,874
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: 10/963,115
/ PRIOR FILING DATE: 2004-10-12
/ PRIOR APPLICATION NUMBER: 60/510,620
/ PRIOR FILING DATE: 2003-10-10
/ PRIOR APPLICATION NUMBER: 60/528,647
/ PRIOR FILING DATE: 2003-12-11

; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 14
 ; LENGTH: 160
 ; TYPE: PRT
 ; ORGANISM: Rhesus monkey
 US-11-010-874-14

Query Match 58.2%; Score 896; DB 7; Length 160;
 Best Local Similarity 93.8%; Pred. No. 5.7e-67;
 Matches 150; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 CKTGNGKRYRGITGMSKTNGITCQKWSSTSPHRPRSPATHPSEGLSENYCRNPDPQGP 65
 DB 1 CKTGNGKRYRGITGMSKTNGITCQKWSSTSPHRPRSPATHPSEGLSENYCRNPDPQGP 60
 QY 66 WCYTDPKRRDYCDILCEBECMHGSGENYDGIKSTMSGLECOAMDOSPHAGYIPS 125
 DB 61 WCYTDPKRRDYCDILCEBECMHGSGENYDGIKSTMSGLECOAMDOSPHAGYIPS 120
 QY 126 KFPNKLKKNYCRNPDRRLRPMWCTTDPNKRWELCDIPRC 165
 DB 121 KFPNKLKKNYCRNPDRRLRPMWCTTDPNKRWELCDIPRC 160

RESULT 15
 US-11-010-874-10
 ; Sequence 10, Application US/11010874
 ; Publication No. US20050250694A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ma, Jian-Xing
 ; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
 ; TITLE OF INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME
 ; FILE REFERENCE: 5820.656
 ; CURRENT APPLICATION NUMBER: US/11/010,874
 ; CURRENT FILING DATE: 2004-12-13
 ; PRIOR APPLICATION NUMBER: 10/963,115
 ; PRIOR FILING DATE: 2004-10-12
 ; PRIOR APPLICATION NUMBER: 60/510,620
 ; PRIOR FILING DATE: 2003-10-10
 ; PRIOR APPLICATION NUMBER: 60/528,647
 ; PRIOR FILING DATE: 2003-12-11
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 10
 ; LENGTH: 168
 ; TYPE: PRT
 ; ORGANISM: porcine
 US-11-010-874-10

Query Match 57.3%; Score 883; DB 7; Length 168;
 Best Local Similarity 84.5%; Pred. No. 6.9e-66;
 Matches 142; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 88 CMHSGENYDGIKSTMSGLECOAMDOSPHAGYIPSKFPNKLKKNYCRNPDRRLRPM 147
 DB 1 CMHSGENYDGIKSTMSGLECOAMDOSPHAGYIPSKFPNKLKKNYCRNPDRRLRPM 60
 QY 148 CFTTDPNKRWELCDIPRCCTTTPPSGPTYQCLKGTSENYRGNVAVTVSQHTCOHWSAQTP 207
 DB 61 CFTTDPNKRWELCDIPRCCTTTPPSGPTYQCLKGTSENYRGNVAVTVSQHTCOHWSAQTP 120
 QY 208 HTHERTPENPCNLDENTCRNPDKKAPWCHTTNSQVMEYCKIPSC 255
 DB 121 HXKNRTPENPCNLDENTCRNPDKKAPWCHTTNSQVMEYCKIPSC 168

Search completed: January 25, 2006, 17:22:35
 Job time : 33 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 25, 2006, 17:01:00 ; Search time 161 Seconds

(without alignments)
1139.362 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540
Sequence: 1 VYLSEKTKNGKNGYGTMSK:.....TNSQVRWEYCKIPSCDSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: uniprot_05.80:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Query Length | DB ID | Description |
|------------|--------|-------------|--------------|-------|--------------|
| 1 | 1535 | 99.7 | 810 | 1 | PLMN_HUMAN |
| 2 | 1535 | 99.7 | 810 | 1 | OSTEH4_HUMAN |
| 3 | 1458 | 94.7 | 810 | 2 | OSR8X6_PONPY |
| 4 | 1442 | 93.6 | 810 | 1 | PLMN_MACMO |
| 5 | 1306 | 84.8 | 359 | 2 | Q8WNR1_CANFA |
| 6 | 1299 | 84.4 | 812 | 1 | PLMN_RAT |
| 7 | 1299 | 84.4 | 812 | 2 | Q5BKB6_RAT |
| 8 | 1292 | 83.9 | 790 | 1 | PLMN_PIG |
| 9 | 1291 | 83.8 | 812 | 1 | PLMN_BOVIN |
| 10 | 1279 | 83.1 | 466 | 2 | Q6TCT0_MOUSE |
| 11 | 1279 | 83.1 | 812 | 1 | PLMN_MOUSE |
| 12 | 1237 | 80.3 | 810 | 1 | PLMN_BRIEU |
| 13 | 1203.5 | 78.1 | 759 | 2 | Q7TP84_RAT |
| 14 | 1160 | 75.3 | 806 | 1 | PLMN_MACRU |
| 15 | 996 | 64.7 | 818 | 2 | Q6PBA6_BRARE |
| 16 | 962 | 62.5 | 797 | 2 | Q50LGE_ORYLA |
| 17 | 959 | 62.3 | 814 | 2 | Q5DVP8_ONCMY |
| 18 | 881 | 57.2 | 2869 | 2 | Q28398_BRIEU |
| 19 | 809.5 | 52.6 | 449 | 2 | Q6GPI4_XENLA |
| 20 | 809.5 | 52.6 | 716 | 2 | Q91691_XENLA |
| 21 | 797 | 51.8 | 708 | 1 | HGR_HUMAN |
| 22 | 796 | 51.7 | 729 | 2 | Q7ZTN9_XENLA |
| 23 | 795.5 | 51.7 | 717 | 2 | P70006_XENLA |
| 24 | 782 | 50.8 | 728 | 1 | HGR_RAT |
| 25 | 778 | 50.5 | 726 | 2 | Q90578_CHICK |
| 26 | 778 | 50.5 | 730 | 2 | Q863B7_CANFA |
| 27 | 777 | 50.5 | 728 | 2 | Q8C9G5_MOUSE |
| 28 | 776.5 | 50.4 | 710 | 2 | Q91402_9R1PI |
| 29 | 776 | 50.4 | 728 | 1 | HGR_MOUSE |
| 30 | 776 | 50.4 | 728 | 2 | Q53WS5_MOUSE |
| 31 | 774 | 50.3 | 730 | 2 | Q76BS1_BOVIN |

| | | | | | | |
|----|-------|------|------|---|--------------|---------------------|
| 32 | 772 | 50.1 | 704 | 2 | Q90865_CHICK | Q90865 gallus gall |
| 33 | 772 | 50.1 | 728 | 2 | Q9BH09_FELCA | Q9BH09 felis silve |
| 34 | 766.5 | 49.8 | 699 | 2 | Q5RGC3_BRARE | Q5RGC3 brachydantio |
| 35 | 766.5 | 49.8 | 709 | 2 | Q90ZNG_BRARE | Q90ZNG brachydantio |
| 36 | 766.5 | 49.8 | 709 | 2 | Q5XFY1_BRARE | Q5XFY1 brachydantio |
| 37 | 766.5 | 49.8 | 716 | 2 | P70521_RAT | P70521 rattus norv |
| 38 | 758 | 49.2 | 655 | 2 | Q4RX92_TETNG | Q4RX92 tetradon n |
| 39 | 754.5 | 49.0 | 405 | 2 | Q788Q2_CHICK | Q788Q2 gallus gall |
| 40 | 753.5 | 48.9 | 716 | 1 | HGR1_MOUSE | P26328 mus musculu |
| 41 | 753.5 | 48.9 | 716 | 2 | Q6GT1L_MOUSE | Q6GT1L mus musculu |
| 42 | 753.5 | 48.9 | 716 | 2 | Q91XG8_MOUSE | Q91XG8 mus musculu |
| 43 | 752 | 48.8 | 667 | 2 | Q4SUG4_TETNG | Q4SUG4 tetradon n |
| 44 | 749 | 48.6 | 2040 | 2 | Q5VTD7_HUMAN | Q5VTD7 homo sapien |
| 45 | 749 | 48.6 | 4548 | 1 | AP0A_HUMAN | P08519 homo sapien |

ALIGNMENTS

| RESULT 1 | ID | PLMN_HUMAN | STANDARD | PRT | 810 AA. |
|----------|--|-----------------------------------|----------|-----|---------|
| AC | P00747 | Q15146 | Q6PA00 | | |
| DT | 21-JUL-1986 | (Rel. 01, Created) | | | |
| DT | 01-MAR-1989 | (Rel. 10, Last sequence update) | | | |
| DT | 13-SEP-2005 | (Rel. 48, Last annotation update) | | | |
| DE | Plasminogen precursor (EC 3.4.21.7) [contains: Plasmin heavy chain A; Activation peptide; Angiotensin; Plasmin heavy chain B, short form; DE Plasmin light chain B]. | | | | |
| GN | Name=PLG; | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Euarchontoglires; Primates; Carnivora; Homnidae; | | | | |
| OC | Homnidae. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RN | [1] | | | | |
| RP | NUCLEOTIDE SEQUENCE, AND VARIANT ASN-472. | | | | |
| RX | MEDLINE=9002879; PubMed=2318648; | | | | |
| RA | Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.; | | | | |
| RT | "Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolytic system." | | | | |
| RL | J. Biol. Chem. 265:6104-6111(1990). | | | | |
| RN | [2] | | | | |
| RP | NUCLEOTIDE SEQUENCE. | | | | |
| RX | MEDLINE=87162490; PubMed=3030813; DOI=10.1016/0014-5793(87)81501-6; | | | | |
| RA | Forrester M., Raden B., Israelson M., Larsson K., Heden L.-O.; | | | | |
| RT | "Molecular cloning and characterization of a full-length cDNA clone for human plasminogen." | | | | |
| RL | FEBS Lett. 213:254-260(1987). | | | | |
| RN | [3] | | | | |
| RP | NUCLEOTIDE SEQUENCE. | | | | |
| RC | TISSUE=Liver; | | | | |
| RA | Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.; | | | | |
| RT | Mitchell D., Robinson J.H.; | | | | |
| RL | "Expression of recombinant human plasminogen and aglycoplasminogen in HeLa cells." | | | | |
| RN | Submitted (Oct-1991) to the EMBL/Genbank/DBJ databases. | | | | |
| RP | [4] | | | | |
| RX | NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS LYS-57; GLN-133; | | | | |
| RA | HIS-261; TRP-408; ASN-472; VAL-494 AND TRP-523. | | | | |
| RT | Rieder M.J., Armel T.Z., Garrington D.P., Osuna M., Kildanek S.A.; | | | | |
| RL | Rafkumar N., Toth E.J., Yi Q., Nickerson D.A.; | | | | |
| RT | "SealSealNPB, NHBIT HL66682 program for genomic applications, UW-Seattle, Seattle, WA (URL: http://pga.gs.washington.edu)." | | | | |
| RN | Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases. | | | | |
| RP | [5] | | | | |
| RX | NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]. | | | | |
| RA | TISSUE=Kidney; | | | | |
| RL | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899; | | | | |
| RA | Strusberg R.V., Feingold E.A., Grose L.H., Derge J.G.; | | | | |
| RT | Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.; | | | | |
| RL | Alteich S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.; | | | | |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.; | | | | |

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stjepic M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Teshlyuk S., Carrion P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RP PROTEIN SEQUENCE OF 20-810, AND VARIANT ASN-472.
 RA Sottrup-Jensen L., Petersen T.E., Magnusson S.,
 RL Submitted (JUL-1977) to the PIR data bank.
 [7]
 RP NUCLEOTIDE SEQUENCE OF 292-810.
 RA MEDLINE=85023311; PubMed=6148961;
 RA Malinowski D.P., Sadler J.E., Davie E.W.,
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 RT human and bovine plasminogen.",
 RL Biochemistry 23:4243-4250(1984).
 [8]
 RP PROTEIN SEQUENCE OF 20-100.
 RA MEDLINE=75093329; PubMed=122932;
 RA Wiman B., Wallen P.,
 RT "Structural relationship between 'glutamic acid' and 'lysine' forms of
 RT human plasminogen and their interaction with the NH2-terminal
 RT activation peptide as studied by affinity chromatography.",
 RL Eur. J. Biochem. 50:489-494(1975).
 [9]
 RP PROTEIN SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810, AND VARIANT
 RA ASN-472.
 RA Sottrup-Jensen L., Claess H., Zajdel M., Petersen T.E., Magnusson S.,
 RT "The primary structure of human plasminogen.",
 RL (in) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);
 RL Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,
 RL Raven Press, New York (1978).
 [10]
 RP PROTEIN SEQUENCE OF 483-604.
 RA MEDLINE=76043692; PubMed=126863;
 RA Wiman B., Wallen P.,
 RT "Amino-acid sequence of the cyanogen-bromide fragment from human
 RT plasminogen that forms the linkage between the plasmin chains.",
 RL Eur. J. Biochem. 58:539-547(1975).
 [11]
 RP PROTEIN SEQUENCE OF 581-810.
 RA MEDLINE=7725245; PubMed=142009;
 RA Wiman B.,
 RT "Primary structure of the B-chain of human plasmin.",
 RL Eur. J. Biochem. 76:129-137(1977).
 [12]
 RP ACTIVE SITE.
 RA MEDLINE=73149248; PubMed=4694729;
 RA Robbins K.C., Bernabe P., Arrazon L., Summaria L.,
 RT "The primary structure of human plasminogen. II. The histidine loop of
 RT human plasmin: light (B) chain active center histidine sequence.",
 RL J. Biol. Chem. 248:1631-1633(1973).
 [13]
 RP ACTIVE SITE.
 RA MEDLINE=69234739; PubMed=4240117;
 RA Groskopf W.R., Summaria L., Robbins K.C.,
 RT "Studies on the active center of human plasmin. Partial amino acid
 RT sequence of a peptide containing the active center serine residue.",
 RL J. Biol. Chem. 244:3590-3597(1969).
 [14]
 RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
 RA MEDLINE=82213905; PubMed=6919539;

RA Trexler M., Vail Z., Patchy L.,
 RT "Structure of the omega-aminocarboxylic acid-binding sites of human
 RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
 RT binding of ligand by kringle 4.",
 RL J. Biol. Chem. 257:7401-7406(1982).
 [15]
 RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
 RA MEDLINE=85054794; PubMed=6094526;
 RA Vail Z., Patchy L.,
 RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34 are
 RT essential for fibrin affinity of the kringle 1 domain.",
 RL J. Biol. Chem. 259:13690-13694(1984).
 [16]
 RP PHOSPHORYLATION SITE SER-597.
 RA MEDLINE=97345939; PubMed=9201958; DOI=10.1021/bi970328d;
 RA Wang H., Protok M., Bretthauer R.K., Castellino F.J.,
 RT "Serine-578 is a major phosphorylation locus in human plasma
 RT plasminogen.",
 RL Biochemistry 36:8100-8106(1997).
 [17]
 RP CARBOHYDRATE-LINKAGE SITES.
 RA MEDLINE=88185329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamberling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegenhart J.F.,
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 RT plasminogen. Species specificity in relation to sialylation and
 RT fucosylation patterns.",
 RL Eur. J. Biochem. 173:57-63(1988).
 [18]
 RP CARBOHYDRATE-LINKAGE SITE SER-268.
 RA MEDLINE=97207306; PubMed=9054441; DOI=10.1074/jbc.272.11.7408;
 RA Pirte-Shepherd S.R., Stevens R.D., Andon N.L., Englund J.J.,
 RA Pizzo S.V.,
 RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
 RT human plasminogen 2.",
 RL J. Biol. Chem. 272:7408-7411(1997).
 [19]
 RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL PROTEIN SEQUENCE.
 RA MEDLINE=95042728; PubMed=7525077; DOI=10.1016/0092-8674(94)90200-3;
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
 RA Moses M.S., Lane W.S., Cao Y., Sage E.H., Folkman J.,
 RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
 RT suppression of metastases by a Lewis lung carcinoma.",
 RL Cell 79:315-328(1994).
 [20]
 RP CHARACTERIZATION OF ANGIOSTATIN.
 RA MEDLINE=97238710; PubMed=9102221;
 RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
 RA Lapevich R., Nacy C.A.,
 RT "A recombinant human angiostatin protein inhibits experimental primary
 RT and metastatic cancer.",
 RL Cancer Res. 57:1329-1334(1997).
 [21]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
 RA MEDLINE=92031502; PubMed=1657148;
 RA Mulichak A.M., Tullinsky A., Ravichandran K.G.,
 RT "Crystal and molecular structure of human plasminogen kringle 4
 RT refined at 1.9-A resolution.",
 RL Biochemistry 30:10576-10586(1991).
 [22]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
 RA MEDLINE=92031503; PubMed=1657149;
 RA Wu T.-P., Padmanabhan K., Tullinsky A., Mulichak A.M.,
 RT "The refined structure of the epsilon-aminocaproic acid complex of
 RT human plasminogen kringle 4.",
 RL Biochemistry 30:10589-10594(1991).
 [23]
 RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
 RA PubMed=15299951; DOI=10.1107/S0907444996012267;
 RA Stec B., Yamano A., Whitlow M., Teeter M.M.,
 RT "Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K.
 RT A possible structural role of disordered residues.",
 RL Acta Crystallogr. D 53:169-178(1997).

RN [24]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.

Query Match 99.7%; Score 1535; DB 1; Length 810;
Best Local Similarity 99.6%; Pred. No. 2.4e-108;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSCKTGNGKNGYGTGSKTKNGITCQKMSSTSPHPPSPATPSEGLSENYCENPN 60
DB 98 VLSCKTGNGKNGYGTGSKTKNGITCQKMSSTSPHPPSPATPSEGLSENYCENPN 157
QY 61 DPQGWCTTDPDEKRYDYCDILECEBCHGSGENYDGKISKTMGLBQAWDSQSPH 120
DB 158 DPQGWCTTDPDEKRYDYCDILECEBCHGSGENYDGKISKTMGLBQAWDSQSPH 217
QY 121 GYIPSKFPNKNLKKNYCRNPDBELRPWCFTTDPNKRWEICDIPRCTPPSSGPTYQCL 180
DB 218 GYIPSKFPNKNLKKNYCRNPDBELRPWCFTTDPNKRWEICDIPRCTPPSSGPTYQCL 277
QY 181 GGENYRGNAVATVSGHTCOHWSAOTPHTHRTPENPCNDENYCRNPDGRAPWCHT 240
DB 278 GGENYRGNAVATVSGHTCOHWSAOTPHTHRTPENPCNDENYCRNPDGRAPWCHT 337
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 2

OSTEH4 HUMAN
ID OSTEH4_HUMAN PRELIMINARY; PRT; 810 AA.

AC OSTEH4_1
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE PlasmaInogen.
GN Name=PLG; ORFNames=RP1-81D8.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL109933; CAI22908.1; -; Genomic_DNA.
DR SMR; OSTEH4; 562-810.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004283; F:plasma activity; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0050874; P:organismal physiological process; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR011358; Pept_S1A_plaamin.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PIRSF; PIRSF001150; PlasmaIn. 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO1505; PROTHROMBIN.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; Tryp_Spc; 1.

DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00948; PAN; 1.

DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW HydroLase; Kringle; Protease; Repeat; Serine protease.
SQ SEQUENCE 810 AA; 90569 MW; 8B31CB877C3BAB6 CRC64;

Query Match 99.7%; Score 1535; DB 2; Length 810;
Best Local Similarity 99.6%; Pred. No. 2.4e-108;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSCKTGNGKNGYGTGSKTKNGITCQKMSSTSPHPPSPATPSEGLSENYCENPN 60
DB 98 VLSCKTGNGKNGYGTGSKTKNGITCQKMSSTSPHPPSPATPSEGLSENYCENPN 157
QY 61 DPQGWCTTDPDEKRYDYCDILECEBCHGSGENYDGKISKTMGLBQAWDSQSPH 120
DB 158 DPQGWCTTDPDEKRYDYCDILECEBCHGSGENYDGKISKTMGLBQAWDSQSPH 217
QY 121 GYIPSKFPNKNLKKNYCRNPDBELRPWCFTTDPNKRWEICDIPRCTPPSSGPTYQCL 180
DB 218 GYIPSKFPNKNLKKNYCRNPDBELRPWCFTTDPNKRWEICDIPRCTPPSSGPTYQCL 277
QY 181 GGENYRGNAVATVSGHTCOHWSAOTPHTHRTPENPCNDENYCRNPDGRAPWCHT 240
DB 278 GGENYRGNAVATVSGHTCOHWSAOTPHTHRTPENPCNDENYCRNPDGRAPWCHT 337
QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 3

Q5R8X6 PONPY
ID Q5R8X6_PONPY PRELIMINARY; PRT; 810 AA.

AC Q5R8X6_1
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp470G2422.
GN Name=DKFZp470G2422;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG The German cDNA Consortium;
RA Pousetka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amd C., Osanger A., Fobz G., Han M., Wilemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CB859622; CH91784.1; -; mRNA.
DR SMR; Q5R8X6; 185-352; 564-810.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004283; F:plasma activity; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0050874; P:organismal physiological process; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR011358; Pept_S1A_plaamin.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.

DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; Trypsin; 1.
 DR PIRSF; PIRSF001150; Plasmin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00948; PAN; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Hypothetical protein; Kringle; Protease; Repeat;
 KM Serine protease.
 SQ SEQUENCE 810 AA; 90380 MW; 126D530C942ADD4 CRC64;

Query Match 94.7%; Score 1458; DB 2; Length 810;
 Best Local Similarity 95.0%; Pred. No. 1.7e-102;
 Matches 247; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 VLSCKTGNGKNVYGTGMSKTNGITCKQWSTSPHPRPSPATPSBGLSENYCRNPDN 60
 DB 98 VLSCKTGNGKNVYGTGMSKTNGITCKQWSTSPHPRPSPATPSBGLSENYCRNPDN 157

QY 61 DPQGMVCTTDEPKRYDCDILCEBECNHCSENGYDKISKTMGLCEQANDSQSPH 120
 DB 158 DAQGMVCTTDEPKRYDCDILCEBECNHCSENGYDKISKTMGLCEQANDSQSPH 217

QY 121 GYIPSPKPKNKLKRYCGRPDDELPRWCCTTPPNKRMELCDIPRCTPPSSGPTTYQCLK 180
 DB 218 GYIPSPKPKNKLKRYCGRPDDELPRWCCTTPPNKRMELCDIPRCTPPSSGPTTYQCLK 277

QY 181 GTGENYRGVAATVSGTQCHWSAOTPHHERTPENFPCKNDENYCRNPDGKRAPWCHT 240
 DB 278 GTGENYRGVAATVSGTQCHWSAOTPHHERTPENFPCKNDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVMEYCKIPSCDSSPV 260
 DB 338 TNSQVMEYCKIPSCDSSPV 357

RESULT 4
 PLAN MACMU STANDARD; PRT; 810 AA.
 ID PLAN MACMU
 AC P12545;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7) [contains: Plasmin heavy chain A;
 DE Activation peptide; Plasmin heavy chain A, short form; Plasmin light
 DE chain B].
 GN Name:Plg;
 OS Macaca mulatta (Rhesus macaque).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCBI_Taxid=9544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=89174660; PubMed=2925643;
 RA Tomlinson J.E., McLean J.W., Lawn R.M.;
 RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
 RT synthesis.",
 RL J. Biol. Chem. 264:5957-5965(1989).
 CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion, and
 CC inflammation; in ovulation it weakens the walls of the Graafian

CC follicle. It activates the urokinase-type plasminogen activator,
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 CC Willebrand factor.
 CC CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa -> Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen
 CC activators, both plasminogen and its activator being bound to
 CC fibrin. Activated with catalytic amounts of streptokinase.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: In the presence of the inhibitor, the activation involves
 CC only cleavage after Arg-560, yielding two chains held together by
 CC two disulfide bonds. In the absence of the inhibitor, the
 CC activation involves additionally the removal of the activation
 CC peptide (by similarity).
 CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
 CC subfamily.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 CC -1- SIMILARITY: Contains 1 PAN domain.
 CC -1- SIMILARITY: Contains 1 peptidase S1 domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; J04697; AAA36901.1; -; mRNA.
 CC PIR; B32869; B30848.
 CC HSSP; P00747; 1BUI.
 CC SMR; P12545; 184-352, 564-810.
 CC MEROPS; S01.233; -;
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR003014; PAN.
 CC InterPro; IPR003609; Pan APP.
 CC InterPro; IPR011358; Pept S1A plasmin.
 CC InterPro; IPR001254; Peptidase_S1_S6.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC InterPro; IPR003966; Peptidase_S1A_pr.
 CC Pfam; PF00051; Kringle; 5.
 CC Pfam; PF00024; PAN; 1.
 CC Pfam; PF00089; Trypsin; 1.
 CC PIRSF; PIRSF001150; Plasmin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR01505; PROTHROMBIN.
 CC ProDom; PD000395; Kringle; 5.
 CC SMART; SM00473; PAN_AP; 1.
 CC SMART; SM00020; TRYP_SPC; 1.
 CC PROSITE; PS00021; KRINGLE_1; 5.
 CC PROSITE; PS00070; KRINGLE_2; 5.
 CC PROSITE; PS00948; PAN; 1.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Blood coagulation; Fibrinolysis; Glycoprotein; Hydrolase; Kringle;
 CC Plasma; Protease; Repeat; Serine protease; Signal; Tissue remodeling;
 CC Zymogen.
 CC KW SIGNAL.
 CC FT CHAIN 1 19
 CC FT CHAIN 20 810 Plasminogen.
 CC FT CHAIN 20 560 Plasmin heavy chain A.
 CC FT PEPTIDE 20 96 Activation peptide.
 CC FT CHAIN 97 580 Plasmin heavy chain A, short form.
 CC FT CHAIN 581 810 Plasmin light chain B.
 CC FT DOMAIN 20 98 PAN.
 CC FT DOMAIN 103 181 Kringle 1.
 CC FT DOMAIN 144 262 Kringle 2.
 CC FT DOMAIN 275 352 Kringle 3.
 CC FT DOMAIN 377 454 Kringle 4.

```

FT DOMAIN 481 560 Kringles 5.
FT DOMAIN 581 808 Peptidase S1.
FT ACT_SITE 622 622 Charge relay system.
FT ACT_SITE 665 665 Charge relay system.
FT ACT_SITE 760 760 Charge relay system.
FT BINDING 134 134 Fibrin.
FT BINDING 136 136 Fibrin.
FT BINDING 136 136 Omega-aminocarboxylic acids.
FT BINDING 158 158 Omega-aminocarboxylic acids.
FT BINDING 172 172 Omega-aminocarboxylic acids.
FT BINDING 432 432 Omega-aminocarboxylic acids.
FT BINDING 445 445 Omega-aminocarboxylic acids.
FT CARBOXHD 365 365 O-linked (GalNac... ) (By similarity).
FT DISULFID 49 73 By similarity.
FT DISULFID 53 61 By similarity.
FT DISULFID 103 181 By similarity.
FT DISULFID 124 164 By similarity.
FT DISULFID 152 176 By similarity.
FT DISULFID 185 262 By similarity.
FT DISULFID 188 216 By similarity.
FT DISULFID 206 245 By similarity.
FT DISULFID 234 257 By similarity.
FT DISULFID 275 352 By similarity.
FT DISULFID 296 335 By similarity.
FT DISULFID 324 347 By similarity.
FT DISULFID 377 454 By similarity.
FT DISULFID 398 437 By similarity.
FT DISULFID 426 449 By similarity.
FT DISULFID 481 560 By similarity.
FT DISULFID 502 543 By similarity.
FT DISULFID 531 555 By similarity.
FT DISULFID 567 685 Interchain (between A and B chains) (By similarity).
FT DISULFID 577 585 Interchain (between A and B chains) (By similarity).
FT DISULFID 607 623 By similarity.
FT DISULFID 699 766 By similarity.
FT DISULFID 729 745 By similarity.
FT DISULFID 756 784 By similarity.
SQ SEQUENCE 810 AA; 90255 MW; A75E1CS1A1A0F24A CRC64;

Query Match 93.6%; Score 1442; DB 1; Length 810;
Best Local Similarity 93.1%; Pred. No. 2.8e-101;
Matches 242; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 YLSECKTGNGKNGYGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLSENYCRNP 60
DB 98 YLSECKTGNGKNGYGTMSKTKRTGTCQKWSSTSPHRPRFSPATHPSEGLSENYCRNP 157

QY 61 DPGWCCTTDPBEKRYDYCDILECEBECMHGSGENYDGKISTKMSGLECOANDSOPHAH 120
DB 158 DPGWCCTTDPBEKRYDYCDILECEBECMHGSGENYDGKISTKMSGLECOANDSOPHAH 217

QY 121 GIYPSKFPNKLKKNYCNRPDLRPMWCTTDPNKRWELCDIPRCTPPSPSGPTYQCLK 180
DB 218 GIYPSKFPNKLKKNYCNRPDLRPMWCTTDPNKRWELCDIPRCTPPSPSGPTYQCLK 277

QY 181 GTGENYRGNAVAVTSGHTCQHSAGTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
DB 278 GTGENYRGNAVAVTSGHTCQHSAGTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 337

QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 338 TNSQVRWEYCKIPSCDSSPV 357

RESULT 5
Q8WR1_CANFA PRELIMINARY; PRT; 359 AA.
AC Q8WR1;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

```

```

DE Plasminogen (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Placentalia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pille-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O.,
RA Folkman J., Waters D.J.; to the EMBL/GenBank/DBJ databases.
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY069985; AAL8519.1; -, mRNA.
DR HSSP; P00747; 1PMK.
DR SMR; Q8WR1; 87-255.
DR Ensembl; ENSCARG0000000759; Canis familiaris.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0003809; F:fibrinogen binding; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000001; Kringles.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; Kringles; 4.
DR PRINTS; PR00018; KRINGLES.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringles; 4.
DR SMART; SM00130; KR; 4.
DR PROSITE; PS00021; KRINGLES_1; 4.
DR PROSITE; PS00070; KRINGLES_2; 4.
FT KRINGLE.
FT NON_TER.
FT NON_TER 1 1
SQ SEQUENCE 359 AA; 41172 MW; 776D35F4AB0BD9E CRC64;

Query Match 84.8%; Score 1306; DB 2; Length 359;
Best Local Similarity 81.2%; Pred. No. 2.6e-91;
Matches 211; Conservative 23; Mismatches 26; Indels 0; Gaps 0;

QY 1 YLSECKTGNGKNGYGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLSENYCRNP 60
DB 1 YLSECKTGNGKNGYGTMSKTKNDVACQKWSSTSPHRPRFSPATHPSEGLSENYCRNP 60

QY 61 DPGWCCTTDPBEKRYDYCDILECEBECMHGSGENYDGKISTKMSGLECOANDSOPHAH 120
DB 61 DPGWCCTTDPBEKRYDYCDILECEBECMHGSGENYDGKISTKMSGLECOANDSOPHAH 120

QY 121 GIYPSKFPNKLKKNYCNRPDLRPMWCTTDPNKRWELCDIPRCTPPSPSGPTYQCLK 180
DB 121 GIYPSKFPNKLKKNYCNRPDLRPMWCTTDPNKRWELCDIPRCTPPSPSGPTYQCLK 180

QY 181 GTGENYRGNAVAVTSGHTCQHSAGTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240
DB 181 GTGENYRGNAVAVTSGHTCQHSAGTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCDSSPV 260
DB 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 6
PLMN_RAT STANDARD; PRT; 812 AA.
ID PLMN_RAT
AC 001177; Q8R0W3;
DT 01-APR-1993 (Rel. 25, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Plasminogen precursor (BC 3.4.21.7) (Contains: Plasmin heavy chain A;
DE Activation peptide; Angiotensin; Plasmin heavy chain A, short form;
DE Plasmin light chain B).
GN Name=Pig;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.

```

OK NCBI_TaxID=10116;
 RN [1]
 RC NUCLEOTIDE SEQUENCE.
 RA TISSUE: Liver;
 RA Bangert K.; Johnsen A.H.; Thorsen S.;
 RA "Rat plasminogen: cDNA and gene structure";
 RA Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RC NUCLEOTIDE SEQUENCE OF 343-511.
 RC TISSUE: Liver;
 RC MEDLINE=91250378; PubMed=1645711;
 RA Kanakas J.J.; Makker S.P.;
 RA "Identification of the rat Heymann nephritis autoantigen (GP330) as a
 RA receptor site for plasminogen";
 RA J. Biol. Chem. 266:10825-10829(1991).
 RL J. Biol. Chem. 266:10825-10829(1991).
 CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion, and
 CC inflammation; in ovulation it weakens the walls of the Graafian
 CC follicle. It activates the urokinase-type plasminogen activator,
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 CC Willebrand factor.
 CC -1- FUNCTION: Angiostatin is an angiogenesis inhibitor that blocks
 CC neovascularization and growth of experimental primary and
 CC metastatic tumors in vivo (By similarity).
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa -> Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen
 CC activators, both plasminogen and its activator being bound to
 CC fibrin. Cannot be activated with streptokinase.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: In the presence of the inhibitor, the activation involves
 CC only cleavage after Arg-581, yielding two chains held together by
 CC two disulfide bonds. In the absence of the inhibitor, the
 CC activation involves additionally the removal of the activation
 CC peptide (By similarity).
 CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
 CC subfamily.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 CC -1- SIMILARITY: Contains 1 PAN domain.
 CC -1- SIMILARITY: Contains 1 peptidase S1 domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL: AJ242649; CAB46014.1; -; mRNA.
 DR EMBL: M62832; AAA41884.1; -; mRNA.
 DR PIR: A40522; A40522.
 DR HSSP: P00747; 1PMK.
 DR SMR: O01177; 565-812.
 DR MEROPS: S01.233; -.
 DR Ensembl: ENSRNOG00000017223; Rattus norvegicus.
 DR RGD: 619893; Pig.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR003014; PAN.
 DR InterPro: IPR003609; Pan app.
 DR InterPro: IPR011358; Pept_S1A_plasmin.
 DR InterPro: IPR001254; Peptidase_S1_S6.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR InterPro: IPR003966; Peptidase_S1A_pr.
 DR Pfam: PF000051; Kringle; 5.
 DR Pfam: PF000024; PAN; 1.
 DR Pfam: PF00089; Trypsin; 1.
 DR PIRSF: PIRSF001150; Plasmin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.

DR PRINTS: PR01505; PROTHROMBIN.
 DR ProDom: PD000395; Kringle; 1.
 DR SMART: SM00130; KR; 1.
 DR PROSITE: PS00021; KRINGLE_1; 5.
 DR PROSITE: PS00070; KRINGLE_2; 5.
 DR PROSITE: PS50948; PAN; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Fibrinolysis; Hydrolyase; Kringle; Plasma; Protease;
 KW Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.
 KM Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.
 FT SIGNAL 1
 FT CHAIN 19
 FT CHAIN 20
 FT CHAIN 20
 FT PEPTIDE 20
 FT CHAIN 98
 FT CHAIN 98
 FT CHAIN 582
 FT CHAIN 20
 FT DOMAIN 102
 FT DOMAIN 184
 FT DOMAIN 274
 FT DOMAIN 375
 FT DOMAIN 480
 FT DOMAIN 582
 FT ACT SITE 624
 FT ACT SITE 667
 FT ACT SITE 762
 FT ACT SITE 762
 FT DISULFID 49
 FT DISULFID 53
 FT DISULFID 103
 FT DISULFID 124
 FT DISULFID 152
 FT DISULFID 185
 FT DISULFID 206
 FT DISULFID 234
 FT DISULFID 275
 FT DISULFID 296
 FT DISULFID 324
 FT DISULFID 347
 FT DISULFID 376
 FT DISULFID 397
 FT DISULFID 425
 FT DISULFID 449
 FT DISULFID 481
 FT DISULFID 502
 FT DISULFID 531
 FT DISULFID 568
 FT DISULFID 578
 FT DISULFID 609
 FT DISULFID 701
 FT DISULFID 721
 FT DISULFID 758
 FT CONFLICT 418
 SQ SEQUENCE 812 AA; 90536 MW; 8C703C51410EBC9B CRC64;
 Query Match 84.4%; Score 1299; DB 1; Length 812;
 Best Local Similarity 82.6%; Pred. No. 2, 1e-90;
 Matches 213; Conservative 21; Mismatches 24; Indels 0; Gaps 0;
 QY 1 VYLSECKTGNGKNGYGTMSKTNGITLCKWMSSTSPHRRPSPATPPSGLSENYCRNPDN 60
 DB 98 VYLSECKTGNGKNGYGTMSKTNGITLCKWMSSTSPHRRPSPATPPSGLSENYCRNPDN 157
 QY 61 DPQGWGCTTTPDEKRYDYCDILECEBCHGSGENYDKISKTMSGLSCQANDSGSPNHH 120
 DB 158 DEQGWGCTTTPDQRYDYCNILECEBCHGSGENYDKISKTMSGLSCQANDSGSPNHH 217
 QY 121 GYIPSKFPKKNLKKRYCGRNDELRPWCTTDPNKRWELCDIPRCTTPPSGPTTQCLK 180
 DB 218 GYIPAKFPKKNLKKRYCGRNDELRPWCTTDPNKRWELCDIPRCTTPPSGPTTQCLK 277

[illegible]

| DR | PRINTS; PR000722; CHYMOTRYPSIN. |
|--|--|
| DR <td>PRINTS; PR000108; KRINGLE.</td> | PRINTS; PR000108; KRINGLE. |
| DR <td>PRINTS; PR01505; PROTHROMBIN.</td> | PRINTS; PR01505; PROTHROMBIN. |
| DR <td>SMART; SM00130; KR; 5.</td> | SMART; SM00130; KR; 5. |
| DR <td>SMART; SM00473; PAN AP; 1.</td> | SMART; SM00473; PAN AP; 1. |
| DR <td>SMART; SM00020; TRYD SPEC; 1.</td> | SMART; SM00020; TRYD SPEC; 1. |
| DR <td>PROSITE; PS00021; KRINGLE_1; UNKNOWN_5.</td> | PROSITE; PS00021; KRINGLE_1; UNKNOWN_5. |
| DR <td>PROSITE; PS50070; KRINGLE_2; 5.</td> | PROSITE; PS50070; KRINGLE_2; 5. |
| DR <td>PROSITE; PS50948; PAN; 1.</td> | PROSITE; PS50948; PAN; 1. |
| DR <td>PROSITE; PS50240; TRYPSIN DOM; 1.</td> | PROSITE; PS50240; TRYPSIN DOM; 1. |
| DR <td>PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.</td> | PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1. |
| DR <td>PROSITE; PS00135; TRYPSIN SER; 1.</td> | PROSITE; PS00135; TRYPSIN SER; 1. |
| KW <td>Hydrolase; Kringle; Protease; Repeat; Serine protease.</td> | Hydrolase; Kringle; Protease; Repeat; Serine protease. |
| SEQUENCE | 812 AA; 90536 MW; 8C703C51410BC93E CRC64; |
| Query Match | 84.4%; Score 1299; DB 2; length 812; |
| Best Local Similarity | 82.6%; Pred. No. 2,1e-90; |
| Matches 213; Conservative | 21; Mismatches 24; Indels 0; Gaps 0; |
| QY | 1 VYLSECKTGNGKNTKGTGMSKTGKGTITQKKSSSTSPHPRPRSPATHPSEGLSENYCRNPND 60 |
| DB | 98 VYLSECKTGIGKGRGTGMSKTKGTGVTQKKSDTSPHVPKSPSTHPSEGLSENYCRNPND 157 |
| QY | 61 DPOSPWCYTTDDPEKRYVYCDLLEGESECHSCSGENYDGTSKTMSGLECAAMPQSFAH 120 |
| DB | 158 DEQSPWCYTTDDPDQRYEYCNIPCESECHMYCSGKTEGKLSKTMSGLDCCSPQSFAH 217 |
| QY | 121 GYISKEPPNNKLKKNYCRNPDRLECPWCFPTTDPYKRWELCDIPRCTPPSPSSGPTYQCLK 180 |
| DB | 218 GYIYAKFPKSLKKNYCRNPDRGEPKPCFTTDPKRWELCDIPRCTPPSPSPGPTYQCLK 277 |
| QY | 181 GTGENYGVNAVTVTSGHTCCWMSAQTPHTHERTEPTEPNCNLDENYCRNPDRGRAPWCHT 240 |
| DB | 278 GRGENYGVTVSVTASGKTCQWMSQTPHRRNRTPEPNCNLDENYCRNPDRGRTAPWCHT 337 |
| QY | 241 TNSGVREWEYCKIPSCDSS 258 |
| DB | 338 TDSQLRWEYCEIPSCGSS 355 |
| RESULT 8 | |
| PLAN_PIG | STANDARD; PRT; 790 AA. |
| AC | P06867; |
| DT | 01-JAN-1988 (Rel. 06, Created) |
| DT | 01-FEB-1991 (Rel. 17, Last sequence update) |
| DT | 13-SEP-2005 (Rel. 48, Last annotation update) |
| DE | Plasminogen precursor (EC 3.4.21.7) [Contains: Plasmin heavy chain A; |
| DE | Activation peptide; Plasmin heavy chain A, short form; Plasmin light |
| DE | chain B]. |
| GN | Name=Pig; |
| OS | Sus scrofa (Pig). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; |
| OC | Sus. |
| OX | NCBI_TaxID=9823; |
| RN | [1] |
| RP | PROTEIN SEQUENCE OF 1-560. |
| RA | Schaller J., Marti T., Roesselet S.J., Kaempfer U., Rickli E.B.; |
| RT | "Amino acid sequence of the heavy chain of porcine plasmin. Comparison |
| RT | of the carbohydrate attachment sites with the human and bovine |
| RT | species."; |
| RL | Fibrinolysis 1:91-102(1987). |
| RN | [2] |
| RP | PROTEIN SEQUENCE OF 450-790. |
| RX | MEDLINE=85203907; PubMed=3846533; |
| RA | Marti T., Schaller J., Rickli E.B.; |
| RT | "Determination of the complete amino-acid sequence of porcine |
| RT | miniplasminogen."; |
| RL | Eur. J. Biochem. 149:279-285(1985). |
| RN | [3] |
| RP | CARBOHYDRATE-LINKAGE SITES. |
| RX | MEDLINE=88185329; PubMed=3356193; |

RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
 RA Gervig G.J., van Halbeek H., Vliegenhart J.F.,
 RT "Type N- and O-linked carbohydrate chains of human, bovine and porcine
 RT plasminogen. Species specificity in relation to sialylation and
 RT fucosylation patterns."
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion, and
 CC inflammation; in ovulation it weakens the wall of the Graafian
 CC follicle. It activates the urokinase-type plasminogen activator,
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, chondroitin, laminin and von
 CC Willebrand factor.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen
 CC activators, both plasminogen and its activator being bound to
 CC fibrin. Cannot be activated with streptokinase.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: N-linked glycan contains N-acetylglucosamine, gallic acid and
 CC is core fucosylated. O-linked glycans consist of Gal-GalNAc
 CC disaccharide which is modified with up to 2 sialic acid residues
 CC (microheterogeneity).
 CC -1- PTM: In the presence of the inhibitor, the activation involves
 CC two disulfide bonds. In the absence of the inhibitor, the
 CC activation involves additionally the removal of the activation
 CC peptide (by similarity).
 CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
 CC subfamily.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 CC -1- SIMILARITY: Contains 1 PAN domain.
 CC -1- SIMILARITY: Contains 1 peptidase S1 domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC PIR: S03733; PIRG.
 CC HSSP: P00747; 1BU1.
 CC SMR: P06867; 544-790.
 CC DR MEROPS: S01.233; -.
 CC DR GLYCSuiteDB: P06867; -.
 CC DR InterPro: IPR000001; Kringle.
 CC DR InterPro: IPR003014; PAN.
 CC DR InterPro: IPR003609; Pan_app.
 CC DR InterPro: IPR011358; Pept_S1a_Plasmin.
 CC DR InterPro: IPR011254; Peptidase_S1_S6.
 CC DR InterPro: IPR001314; Peptidase_S1A.
 CC DR InterPro: IPR003966; Peptidase_S1a_pr.
 CC Pfam: PR00051; Kringle; 5.
 CC Pfam: PR00024; PAN; 1.
 CC Pfam: PR00089; Trypsin; 1.
 CC DR PIRSF: PIRSF01150; Plasmin; 1.
 CC DR PRINTS: PR00722; CHYMOTRYPSIN.
 CC DR PRINTS: PR00018; KRINGLE.
 CC DR PRINTS: PR01505; PROTHROMBIN.
 CC DR ProDom: PD000395; Kringle; 5.
 CC DR SMART: SM00130; KR; 5.
 CC DR SMART: SM00473; PAN AP; 1.
 CC DR SMART: SM00020; TRYP_SPC; 1.
 CC DR PROSITE: PS00021; KRINGLE_1; 5.
 CC DR PROSITE: PS50070; KRINGLE_2; 5.
 CC DR PROSITE: PS50948; PAN; 1.
 CC DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 CC DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
 CC DR PROSITE: PS00135; TRYPSIN_SER; 1.

KW Blood coagulation; Direct protein sequencing; Fibrinolysis;
 KW Glycoprotein; Hydrolase; Kringle; Plasma; Protease; Repeat;
 KW Serine protease; Tissue remodeling; Tissue
 FT CHAIN 1 560
 FT PEPTIDE 1 78
 FT CHAIN 79 560
 FT CHAIN 561 790
 FT DOMAIN 1 79
 FT DOMAIN 84 162
 FT DOMAIN 166 243
 FT DOMAIN 256 333
 FT DOMAIN 358 435
 FT DOMAIN 461 540
 FT DOMAIN 561 788
 FT ACT SITE 602 602
 FT ACT SITE 645 645
 FT ACT SITE 740 740
 FT CARBOHYD 289 289
 FT CARBOHYD 340 340
 FT DISULFID 30 54
 FT DISULFID 34 42
 FT DISULFID 84 162
 FT DISULFID 105 145
 FT DISULFID 133 157
 FT DISULFID 166 243
 FT DISULFID 169 297
 FT DISULFID 187 226
 FT DISULFID 215 238
 FT DISULFID 256 333
 FT DISULFID 277 316
 FT DISULFID 305 328
 FT DISULFID 358 435
 FT DISULFID 379 418
 FT DISULFID 407 430
 FT DISULFID 461 540
 FT DISULFID 482 523
 FT DISULFID 511 535
 FT DISULFID 547 665
 FT DISULFID 557 565
 FT DISULFID 587 603
 FT DISULFID 679 746
 FT DISULFID 709 725
 FT DISULFID 736 764
 SQ SEQUENCE 790 AA; 88593 MW; F04EA06574BCD58E CRC64;
 Query Match 83.9%; Score 1292; DB 1; Length 790;
 Best Local Similarity 81.4%; Pred. No. 7.1e-90;
 Matches 210; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYGTMSKTKNGITTCQWMSSTPHRPSPATPSBGLFENYCRNP 60
 DB 79 IYLSCKTGNGKNGYGTMSKTKNGITTCQWMSSTPHRPSPATPSBGLFENYCRNP 138
 QY 61 DPGPWCYTTDPBKKYDYLCEBECMGHSGENYDGKISTKMSGLBEOAMDOSPHAH 120
 DB 139 DKGPGCYTTDPETPFYCDLPECEBCHMGHSGENYEGKISTKMSGIRGOSGSPH 198
 QY 121 GYIPSKFPKNLKNKYCRNPDRLEPWCFTTDPNKRWELCDIPRCTPPSPSGPTQC 180
 DB 199 GYLPKFPKNLKNKYCRNPDRLEPWCFTTDPNKRWELCDIPRCTPPSPSGPTQC 258
 QY 181 GTGENYRGNAVTVSGHTCQWMSAOTPRTHETPPENFPKNTDENTYCRNPDKRAWCHT 240
 DB 259 GGENYRGTVSVTAGHTCQWMSAOSPKNRHTPENFPCKNLBNYCRNPDELTAWCT 318
 QY 241 TNSQVPMWECYKIPSCDS 258
 DB 319 TDSVPMWYCKIPSCDS 336

RESULT 9
 PLMN BOVIN STANDARD; PRT; 812 AA.
 AC P06868; Q28162;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7) [contains: Plasmin heavy chain A; Activation peptide; Plasmin heavy chain A, short form; Plasmin light chain B].
 GN Name=PLG;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 OK (1)
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RA Berglund L., Andersen M.D., Petersen T.E.;
 RT "Cloning and characterization of the bovine plasminogen cDNA."; Int. Dairy J. 5:593-603(1995).
 RL [2]
 RP PROTEIN SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=85203906; PubMed=3846532;
 RA Schaller J., Moser P.W., Danneberger-Muller G.A.K., Rosselet S.J., Kamper U., Rickli E.B.;
 RT "Complete amino acid sequence of bovine plasminogen. Comparison with human plasminogen.";
 RL Eur. J. Biochem. 149:267-278(1985).
 RN [3]
 RP NUCLEOTIDE SEQUENCE OF 706-812.
 RX MEDLINE=85023311; PubMed=618961;
 RA Malinowski D.P., Sadler J.E., Davie E.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen.";
 RL Biochemistry 23:4243-4250(1984).
 RN [4]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli E.B., Schmid K., Kamerling J.P., Gerwig G.J., Van Halbeek H., Vliegenhart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine plasminogen. Species specificity in relation to sialylation and fucosylation patterns.";
 RL Eur. J. Biochem. 173:57-63(1988).
 CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.
 CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: N-linked glycan contains N-acetylglucosamine and sialic acid. O-linked glycans consist of Gal-GalNAc disaccharide which is modified with up to 2 sialic acid residues (microheterogeneity).
 CC -1- PTM: In the presence of the inhibitor, the activation involves only cleavage after Arg-583, yielding two chains held together by two disulfide bonds. In the absence of the inhibitor, the activation involves additionally the removal of the activation peptide (by similarity).
 CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen

CC subfamily.
 CC -1- SIMILARITY: Contains 5 kringle domains.
 CC -1- SIMILARITY: Contains 1 PAN domain.
 CC -1- SIMILARITY: Contains 1 peptidase S1 domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 CC EMBL; X79402; CAA55939.1; -; mRNA.
 CC EMBL; X02935; AAA30714.1; -; mRNA.
 CC PIR; S45046; PLBO.
 CC HSSP; P00747; 2PK4.
 CC SMR; P06868; 191-359, 568-812.
 CC MEROPS; S01.233; -;
 CC GlycoSuiteDB; P06868; -;
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR003014; PAN.
 CC InterPro; IPR003609; Pan_app.
 CC InterPro; IPR011358; Pept_S1A_Plaamin.
 CC InterPro; IPR001254; Peptidase_S1_S6.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC InterPro; IPR003966; Peptidase_S1A_pr.
 CC Pfam; PF00051; Kringle; 5.
 CC Pfam; PF00024; PAN; 1.
 CC Pfam; PF00089; Trypsin; 1.
 CC PIRSF; PIRSF001150; Plasmin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00018; KRINGLE.
 CC PRINTS; PR01505; BROTHROMBIN.
 CC ProDom; PD000395; Kringle; 5.
 CC PROSITE; PS00021; KRINGLE_1; 5.
 CC PROSITE; PS50070; KRINGLE_2; 5.
 CC PROSITE; PS50948; PAN; 1.
 CC PROSITE; PS50240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC DR PROSITE; PS00135; TRYPSIN_SER; 1.
 CC DR Blood coagulation; Direct protein sequencing; Fibrinolysis; KW Glycoprotein; Hydrolyase; Kringle; Plasma; Protease; Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.
 CC FT SIGNAL 1 26
 CC FT CHAIN 27 812 Plasminogen.
 CC FT CHAIN 27 883 Plasmin heavy chain A.
 CC FT PEPTIDE 27 104 Activation peptide (By similarity).
 CC FT CHAIN 105 583 Plasmin heavy chain A, short form (By similarity).
 CC FT CHAIN 584 812 Plasmin light chain B.
 CC FT DOMAIN 29 105 PAN.
 CC FT DOMAIN 110 188 Kringle 1.
 CC FT DOMAIN 192 269 Kringle 2.
 CC FT DOMAIN 282 359 Kringle 3.
 CC FT DOMAIN 384 461 Kringle 4.
 CC FT DOMAIN 485 564 Kringle 5.
 CC FT DOMAIN 584 810 Peptidase S1.
 CC FT ACT_SITE 624 624 Charge relay system.
 CC FT ACT_SITE 667 667 Charge relay system.
 CC FT ACT_SITE 762 762 Charge relay system.
 CC FT CARBOHYD 315 315 N-linked (GlcNAc...)
 CC FT CARBOHYD 315 315 /FTId=CAR_000014.
 CC FT CARBOHYD 365 365 O-linked (GalNAc...)
 CC FT DISULFID 56 80 /FTId=CAR_000015.
 CC FT DISULFID 60 80 By similarity.
 CC FT DISULFID 110 188 By similarity.
 CC FT DISULFID 131 171 By similarity.
 CC FT DISULFID 159 183 By similarity.
 CC FT DISULFID 182 269 By similarity.
 CC FT DISULFID 195 323 By similarity.
 CC FT DISULFID 213 252 By similarity.
 CC FT DISULFID 241 264 By similarity.
 CC FT DISULFID 282 359 By similarity.

RA Nagarsaja R.;
RT "genomic sequence analysis in the mouse t-complex region."
RL Submitted (FEB-2002) to the EMBL/Genbank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Liver.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettner K.H., Schaefer C.F., Bhut N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dapchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedtin T.B., Toehlyuk S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 1-16.
RC STRAIN=129/SvJ; TISSUE=Liver;
RX MEDLINE=22254843; PubMed=12149246; DOI=10.1074/jbc.M202509200;
RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
RA Farmer R.J., Miles L.A.;
RT "Localization of regulatory elements mediating constitutive and
RT cytokine-stimulated plasminogen gene expression.";
RL J. Biol. Chem. 277:38579-38588(2002).
RN [5]
RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=95042728; PubMed=7555077; DOI=10.1016/0092-8674(94)90200-3;
RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma.";
RL Cell 79:315-328(1994).
CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
CC a proteolytic factor in a variety of other processes including
CC embryonic development, tissue remodeling, tumor invasion, and
CC inflammation; in ovulation it weakens the walls of the Graafian
CC follicle. It activates the urokinase-type plasminogen activator,
CC collagenases and several complement zymogens, such as C1 and C5.
CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
CC Willebrand factor.
CC -1- FUNCTION: Angiostatin is an angiogenesis inhibitor that blocks
CC neovascularization and growth of experimental primary and
CC metastatic tumors in vivo.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa > Arg]-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen
CC activators, both plasminogen and its activator being bound to
CC fibrin. Cannot be activated with streptokinase.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PM: In the presence of the inhibitor, the activation involves
CC only cleavage after Arg-581, yielding two chains held together by
CC two disulfide bonds. In the absence of the inhibitor, the
CC activation involves additionally the removal of the activation
CC peptide (by similarity).
CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
CC immediately after dissociation from the clt.
CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC subfamily.
CC -1- SIMILARITY: Contains 5 kringle domains.
CC -1- SIMILARITY: Contains 1 PAN domain.

| | |
|----|--|
| CC | - - SIMILARITY: Contains 1 peptidase S1 domain. |
| CC | ----- |
| CC | This Swiss-Prot entry is copyright. It is produced through a collabora- |
| CC | tion between the Swiss Institute of Bioinformatics and the EMBL outstac- |
| CC | the European Bioinformatics Institute. There are no restrictions on |
| CC | use as long as its content is in no way modified and this statement i |
| CC | removed. |
| CC | ----- |
| DR | EMBL, J04766; AAA50168.1 -; mRNA. |
| DR | EMBL, AF481053; AAM22156.1 -; Genomic_DNA. |
| DR | EMBL, BC014773; AAH14773.1 -; mRNA. |
| DR | EMBL, BC051786; AAH57186.1 -; mRNA. |
| DR | EMBL, AY134430; AAN15805.1 -; Genomic_DNA. |
| DR | PIR, A36514; PLMS. |
| DR | HSSP, P00747; IBIU. |
| DR | SMR, P20918; 184-352, 566-812. |
| DR | MEROPS, S01.233; -. |
| DR | Ensembl: ENSEMBLG00000059481. Mus musculus. |
| DR | MGI, MGI:97620; Pig. |
| DR | GO, GO:0005615; C.eitracellular space; TAS. |
| DR | GO, GO:0006915; P.apoptosis; IDA. |
| DR | GO, GO:0006917; P.induction of apoptosis; IDA. |
| DR | GO, GO:0046716; P.muscle maintenance; IMP. |
| DR | GO, GO:0007519; P.myogenesis; IMP. |
| DR | GO, GO:0016525; P.negative regulation of angiogenesis; TAS. |
| DR | GO, GO:0042246; P.tissue regeneration; IMP. |
| DR | InterPro, IPRO00001; Kringle. |
| DR | InterPro, IPRO03014; PAN. |
| DR | InterPro, IPRO03609; Pan app. |
| DR | InterPro, IPRO11358; Pept_S1A_plasmin. |
| DR | InterPro, IPRO01254; Peptidase_S1_S6. |
| DR | InterPro, IPRO01314; Peptidase_S1A. |
| DR | InterPro, IPRO03966; Peptidase_S1A_pr. |
| DR | Pfam, PF00051; Kringle_5. |
| DR | Pfam, PF00024; PAN_1. |
| DR | Pfam, PF00089; Trypsin_1. |
| DR | PIRSF, PIRSF001150; Plasmin_1. |
| DR | PRINTS, PRO0722; CHYMOTRYPSIN. |
| DR | PRINTS, PRO0018; KRINGLE. |
| DR | PRINTS, PRO1505; PROTHROMBIN. |
| DR | Prodom, PD000395; Kringle_5. |
| DR | PROSITE, PS00021; KRINGLE_1_5. |
| DR | PROSITE, PS50070; KRINGLE_2_5. |
| DR | PROSITE, PS50948; PAN_1. |
| DR | PROSITE, PS50240; TRYPSIN_DOM; 1. |
| DR | PROSITE, PS00134; TRYPSIN_HIS; 1. |
| KM | PROSITE, PS00135; TRYPSIN_SER; 1. |
| KM | Blood coagulation; Direct protein sequencing; Fibrinolysis; Hydrolyase |
| KM | Kringle; Plasmn; Protease; Repeat; Serine protease; Signal; |
| KM | Tissue remodeling; Zymogen. |
| KW | SIGNAL 1 19 |
| FT | CHAIN 20 812 plasmin. |
| FT | CHAIN 20 581 plasmin heavy chain A. |
| FT | PEPTIDE 20 97 Activation peptide. |
| FT | CHAIN 98 581 Angiotensin heavy chain A, short form. |
| FT | CHAIN 98 7436 Angiotensin. |
| FT | CHAIN 582 812 Plasmin light chain B. |
| FT | DOMAIN 20 98 PAN. |
| FT | DOMAIN 103 181 Kringle 1. |
| FT | DOMAIN 184 262 Kringle 2. |
| FT | DOMAIN 275 352 Kringle 3. |
| FT | DOMAIN 377 454 Kringle 4. |
| FT | DOMAIN 481 560 Kringle 5. |
| FT | DOMAIN 582 810 Peptidase_s1. |
| FT | ACT_SITE 624 Charge relay system (By similarity). |
| FT | ACT_SITE 667 Charge relay system (By similarity). |
| FT | ACT_SITE 762 Charge relay system (By similarity). |
| FT | DISULFID 49 73 By similarity. |
| FT | DISULFID 53 61 By similarity. |
| FT | DISULFID 103 181 By similarity. |
| FT | DISULFID 124 164 By similarity. |
| FT | DISULFID 152 176 By similarity. |
| FT | DISULFID 185 262 By similarity. |

```

FT DISULFID 188 316 By similarity.
FT DISULFID 206 245 By similarity.
FT DISULFID 234 257 By similarity.
FT DISULFID 275 352 By similarity.
FT DISULFID 296 335 By similarity.
FT DISULFID 324 347 By similarity.
FT DISULFID 377 454 By similarity.
FT DISULFID 398 437 By similarity.
FT DISULFID 426 449 By similarity.
FT DISULFID 481 560 By similarity.
FT DISULFID 502 543 By similarity.
FT DISULFID 531 555 By similarity.
FT DISULFID 568 687 Interchain (between A and B chains) (By
FT DISULFID 578 586 similarity).
FT DISULFID 609 625 Interchain (between A and B chains) (By
FT DISULFID 701 768 similarity).
FT DISULFID 731 747 By similarity.
FT DISULFID 758 786 By similarity.
FT CONFLICT 225 235 R -> H (in Ref. 1).
FT CONFLICT 525 525 G -> D (in Ref. 1).
FT CONFLICT 649 649 S -> L (in Ref. 1).
SQ SEQUENCE 812 AA; 90782 MW; 241732606A2FFD2 CRC64;

Query Match 83.1%; Score 1279; DB 1; Length 812;
Beet Local Similarity 81.0%; Pred. No. 7, 1e-89;
Matches 209; Conservative 22; Mismatches 27; Indels 0; Gaps 0;

QY 1 VLSSECKTGNGKNGYGTMSKTKNGITCKQMSSTSPHPRFPSPATPSPGLEENYCRNPDN 60
DB 98 VLSSECKTGNGKNGYGTMSKTKNGITCKQMSSTSPHPRFPSPATPSPGLEENYCRNPDN 157
QY 61 DPQGWCTTDDPKRYDYCDIIECEBECMHGCGENTDGKISTKNGSLBQANDSQSPH 120
DB 158 DPQGWCTTDDPKRYDYCDIIECEBECMHGCGENTDGKISTKNGSLBQANDSQSPH 217
QY 121 GYTPKFPKKNKKYKNCRNPRELRPWCFTDPPNKRWELCDIPRCTPPSPSGPTVQCL 180
DB 218 GYTPKFPKKNKKYKNCRNPRELRPWCFTDPPNKRWELCDIPRCTPPSPSGPTVQCL 277
QY 181 GTGENYRGNAVTVSGTQCHNSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCH 240
DB 278 GTGENYRGNAVTVSGTQCHNSAQTPTHTERTPENFPCKNLDENYCRNPDGKRAPWCH 337
QY 241 TNSQVMEYCKIPSCDS 258
DB 338 TDSQLRMEYCEIPIPCSS 355

RESULT 12
PLMN ERIEU STANDARD; PRT; 810 AA.
AC 029485;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Plasmaogen precursor (EC 3.4.21.77) [Contains: Plasmain heavy chain A,
DE Activation peptide; Plasmain heavy chain A, short form; Plasmain light
DE chain B].
GN Name=PIG;
OS Eritaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Insectivora; Erinaceidae;
OC Erinaceinae; Erinaceus.
OC NCBI_TaxID=9365;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96025778; PubMed=7592597; DOI=10.1074/jbc.270.41.24004;
RA Lawn R.M., Boommark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
RA Byrne C.D., Fong K.J., Meer K., Patchy L.;
"the recurring evolution of lipoprotein(a). Insights from cloning of

```

```

RT hedgehog apolipoprotein(a).";
RL J. Biol. Chem. 270:24004-24009 (1995).
RN [2]
RP SEQUENCE REVISION.
RA Lawn R.M.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Plasmain dissolves the fibrin of blood clots and acts as
CC a proteolytic factor in a variety of other processes including
CC embryonic development, tissue remodeling, tumor invasion, and
CC inflammation; in circulation it weakens the walls of the Graafian
CC follicle. It activates the urokinase-type plasminogen activator,
CC collagenase and several complement zymogens, such as C1 and C5.
CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
CC Willbrand factor.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen
CC activators, both plasminogen and its activator being bound to
CC fibrin. Cannot be activated with streptokinase.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: In the presence of the inhibitor, the activation involves
CC only cleavage after Arg-582, yielding two chains held together by
CC two disulfide bonds. In the absence of the inhibitor, the
CC activation involves additionally the removal of the activation
CC peptide (By similarity).
CC -1- MISCELLANEOUS: Plasmain is inactivated by alpha-2-antiplasmin
CC immediately after dissociation from the clot.
CC -1- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
CC subfamily.
CC -1- SIMILARITY: Contains 5 kringle domains.
CC -1- SIMILARITY: Contains 1 PAN domain.
CC -1- SIMILARITY: Contains 1 peptidase S1 domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: U33171, AAC48717.1; -, mRNA.
CC PIR: I46260; I46260.
CC HSSP: P00747; 1B01.
CC SMR: Q29485; 568-810.
CC MEROPS: S01_233; -.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR003014; PAN.
CC InterPro: IPR003609; Pan_app.
CC InterPro: IPR01358; Pept_S1A_Plasmin.
CC InterPro: IPR001254; Peptidase_S1_S6.
CC InterPro: IPR001314; Peptidase_S1A.
CC InterPro: IPR003966; Peptidase_S1A_pr.
CC Pfam: PF00051; Kringle; 5.
CC Pfam: PF00024; PAN; 1.
CC Pfam: PF00089; Trypsin; 1.
CC PIRSF: PIRSF001150; Plasmin; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00018; KRINGLE.
CC PRINTS: PR01505; PROTHROMBIN.
CC ProDom: PD000395; Kringle; 5.
CC SMART: SM00130; KR; 5.
CC SMART: SM00473; PAN_AP; 1.
CC SMART: SM00020; TRYD_SPC; 1.
CC PROSITE: PS00021; KRINGLE_1; 5.
CC PROSITE: PS50070; KRINGLE_2; 5.
CC PROSITE: PS50948; PAN; 1.
CC PROSITE: PS50240; TRYPSIN_DOM; 1.
CC PROSITE: PS00134; TRYPSIN_HIS; 1.
CC PROSITE: PS00135; TRYPSIN_SER; 1.
CC Blood coagulation; Fibrinolysis; Glycoprotein; Hydrolase; Kringle;
CC Plasma; Protease; Repeat; Serine protease; Signal; Tissue remodeling;
CC Zymogen.
FT SIGNAL 1 19 By similarity.

```

| | | | | |
|----|----------|---------|-----------|--|
| FT | CHAIN | 20 | 810 | Plasminogen. |
| FT | CHAIN | 20 | 562 | Plasmin heavy chain A (By similarity). |
| FT | PEPTIDE | 20 | 57 | Activation peptide (By similarity). |
| FT | CHAIN | 98 | 562 | Plasmin heavy chain A, short form (By similarity). |
| FT | CHAIN | 583 | 810 | Plasmin light chain B (By similarity). |
| FT | DOMAIN | 20 | 98 | p1n. |
| FT | DOMAIN | 103 | 181 | Kingle 1. |
| FT | DOMAIN | 185 | 262 | Kingle 2. |
| FT | DOMAIN | 275 | 352 | Kingle 3. |
| FT | DOMAIN | 379 | 456 | Kingle 4. |
| FT | DOMAIN | 482 | 561 | Kingle 5. |
| FT | DOMAIN | 582 | 808 | Peptidase S1. |
| FT | ACT_SITE | 622 | 622 | Charge relay system. |
| FT | ACT_SITE | 665 | 665 | Charge relay system. |
| FT | ACT_SITE | 760 | 760 | Charge relay system. |
| FT | CAROHYD | 339 | 339 | N-linked (GlcNAc. . .) (Potential). |
| FT | DISULFID | 49 | 73 | By similarity. |
| FT | DISULFID | 53 | 61 | By similarity. |
| FT | DISULFID | 103 | 181 | By similarity. |
| FT | DISULFID | 124 | 164 | By similarity. |
| FT | DISULFID | 152 | 176 | By similarity. |
| FT | DISULFID | 185 | 262 | By similarity. |
| FT | DISULFID | 188 | 316 | By similarity. |
| FT | DISULFID | 206 | 245 | By similarity. |
| FT | DISULFID | 234 | 257 | By similarity. |
| FT | DISULFID | 275 | 352 | By similarity. |
| FT | DISULFID | 296 | 335 | By similarity. |
| FT | DISULFID | 324 | 347 | By similarity. |
| FT | DISULFID | 379 | 439 | By similarity. |
| FT | DISULFID | 400 | 439 | By similarity. |
| FT | DISULFID | 428 | 451 | By similarity. |
| FT | DISULFID | 482 | 561 | By similarity. |
| FT | DISULFID | 503 | 544 | By similarity. |
| FT | DISULFID | 532 | 556 | By similarity. |
| FT | DISULFID | 569 | 665 | Interchain (between A and B chains) (By similarity). |
| FT | DISULFID | 579 | 566 | Interchain (between A and B chains) (By similarity). |
| FT | DISULFID | 607 | 623 | By similarity. |
| FT | DISULFID | 699 | 766 | By similarity. |
| FT | DISULFID | 729 | 745 | By similarity. |
| FT | DISULFID | 756 | 784 | By similarity. |
| SQ | SEQUENCE | 810 AA; | 90902 MW; | 8E57580946017A16 CRC64; |

[illegible]

```

AC      Q7TP84; 01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Ab1-346.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN
RP      NUCLEOTIDE SEQUENCE.
RA      Xu C.S., Li W.Q., Li Y.C., Yan H.M., Chang C.F., Zhao L.F., Ma H.,
RA      Wang L., Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yan J.Y.,
RA      Yang K.J., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL      Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AY325159; AAP92560.1; -, mRNA.
DR      HSRP; P00747; Ibut.
DR      SRR; Q7TP84; 83-360, 661-759.
DR      Ensembl; ENSRNOCG0000017223; Rattus norvegicus.
DR      GO; GO:0005509; P:calcium ion binding; IEA.
DR      GO; GO:0008233; P:peptidase activity; IEA.
DR      GO; GO:0003809; F:thrombin activity; IEA.
DR      GO; GO:0004295; F:trypsin activity; IEA.
DR      GO; GO:0007596; P:blood coagulation; IEA.
DR      GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro; IPR000001; Kringle.
DR      InterPro; IPR003014; PAN.
DR      InterPro; IPR013358; Pept_S1A_Plasmin.
DR      InterPro; IPR001254; Peptidase_S1_S6.
DR      InterPro; IPR003966; Peptidase_S1A_pr.
DR      Pfam; PF00051; Kringle; 5.
DR      Pfam; PF00024; PAN; 1.
DR      PIRSF; PIRSF001150; Plasmin; 1.
DR      PRINTS; PR00018; KRINGLE.
DR      PRINTS; PR01505; BROTHOMBIN.
DR      ProDom; PD000395; Kringle; 5.
DR      SMART; SM00130; KR; 5.
DR      SMART; SM00020; TRY_Spc; 1.
DR      PROSITE; PS00021; KRINGLE_1; 5.
DR      PROSITE; PS00070; KRINGLE_2; 5.
DR      PROSITE; PS02403; TRYPSIN_DOM; 1.
DR      PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
SQ      SEQUENCE 759 AA; 86057 MW; 1422BFAC05C5DFA7 CRC64;

```

[illegible]


```

Db      278 GGENYRGKIAVTKSGHTQRMWKOQPHKHNRTPEHFPCRGIDENYCRNPDELEPWCT 337
QY      241 TMSQVMEYCKIPSCDSS 258
Db      338 TNPVROEYCALPSCGTS 355

RESULT 15
Q6PBA6 BRARE
ID Q6PBA6 BRARE PRELIMINARY; PRT; 818 AA.
AC Q6PBA6;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE Plasmimogen.
GN Name=pig;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxId=7955;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059801; AAH59801.1; -, mRNA.
DR HSSP; P00747; 1B21.
DR ZFIN; ZDB-GENE-030131-1411; plg.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:calcium ion binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004283; F:peptidase activity; IEA.
DR GO; GO:0003809; F:plasma activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0050874; P:organismal physiological process; IEA.
DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan. app.
DR InterPro; IPR01358; Pept_SIA_Plaamin.
DR InterPro; IPR01254; Peptidase_S1_S6.
DR InterPro; IPR01314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; Trypsin; 1.

```

```

DR PIRSF; PIRSF001150; Plaamin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR0018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 3.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00948; PAN; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Kringle; Protease; Repeat; Serine protease.
SQ SEQUENCE 818 AA; 91636 MW; 55AC014BA38F778 CRC64;

Query Match          64.7%; Score 996; DB 2; Length 818;
Best Local Similarity 61.2%; Pred. No. 2.4e-67;
Matches 158; Conservative 34; Mismatches 66; Indels 0; Gaps 0;

QY      2 YLSCKTGNGKNTYRGTMSTKNGITTCQKWSSTSPHPRPSPATHPSEGLEENYCRNPND 61
Db      106 YLLEFVNGIGMDYRGTKSKTKSGKTCORWEGTFPHVPIITPRAYPKADLESNFCNPDGD 165
QY      62 PQGPKCTTDPKRYDYGDIILECEHCWCGSENGDKITSKTMSGLEQAMDSOPHANG 121
Db      166 KGGPVCYTTDPKREHCNIDCTECMCQSGENYRGKISTVSGFTQCRMDSQDPONG 225
QY      122 YIPSPKPNKNTLKNTYCRNPDELRPWCFTTDPNKKWELCDIPRCTTPPSGPTVQCLKG 181
Db      226 YLPSLPKXYLEENYCRNPDELRPWCFTTSPSKWELCALPRTCTTEPTIYBELTCSAG 285
QY      182 TGENYRGNVAVTSGTQHSNAQTPTHTERTPENPCKNIDENYCRNPDGRAPWCHTT 241
Db      286 EGSYRGTSVITGKTCQWTSQSPHKSRSPEYPCKGLDGNYCRNPDNERSPWCTTT 345
QY      242 NSQVMEYCKIPSCDSSP 259
Db      346 DPETMEYCSVPSCGDP 363

```

Search completed: January 25, 2006, 17:10:07
 Job time : 163 secs

This Page Blank (uspto)